PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

l	(51) International Part of Cl. 10	T	CADER THE PATENT COOPERATION TREATY (PCT)			
	(51) International Patent Classification 6: C07H 21/00, C12N 1/15, 1/21, 5/10,	A1	(11) International Publication Number:	WO 99/31117		
	15/11, 15/63		(43) International Publication Date:	24 June 1999 (24.06.99)		

(21) International Application Number: PCT/US98/27059
(22) International Filing Date: 17 December 1998 (17.12.98)

(30) Priority Data: 60/070,923 18 December 1997 (18.12.97) US 60/068,007 18 December 1997 (18.12.97) US 60/068,057 18 December 1997 (18.12.97) US 60/068,006 18 December 1997 (18.12.97) US 60/068,008 18 December 1997 (18.12.97) US 60/068,054 18 December 1997 (18.12.97) US 60/068,064 18 December 1997 (18.12.97) US 60/068,053 18 December 1997 (18.12.97) US 60/068,169 19 December 1997 (19.12.97) US 60/068,368 19 December 1997 (19,12,97) US 60/068,367 19 December 1997 (19.12.97) US 60/068,369 19 December 1997 (19.12.97) US 60/068,365 19 December 1997 (19.12.97) US

(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): MOORE, Paul, A. [US/US]; 19005 Leatherbark Drive, Germantown, MD

20874 (US). RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US). SHI, Yang-gu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). SOPPET, Daniel, R. [US/US]; 15050 Stillfield Place, Centreville, VA 22020 (US). KYAW, Hla [MM/US]; 520 Sugarbush Circle, Frederick, MD 21703 (US). WEI, Ying-Fei [CN/US]; 1714-C Marina Court, San Mateo, CA 94403 (US). FLORENCE, Kimberly [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). DUAN, Roxanne, D. [US/US]; 5515 Northfield Road, Bethesda, MD 20817 (US). FLORENCE, Charles [US/US]; 12805 Altantic Avenue, Rockville, MD 20851 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US). FENG, Ping [CN/US]; 4 Relda Court, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 120 Fox Run Drive, Tewksbury, MA 01876 (US). YU, Guo-Liang [CN/US]; 1714-C Marina Court, San Mateo, CA 94403 (US). JANAT, Fouad [SY/US]; 140 High Street, No. 202, Westerly, RI 02891 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US).

(74) Agents: BROOKES, A., Anders et al., Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

With international search report.

(54) Title: 110 HUMAN SECRETED PROTEINS

(57) Abstract

The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	ĹV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	ТJ	Tajikistan
BE	Belgium	GN	Guinea	мк	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA.	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	· VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	zw	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's	NZ	New Zealand		
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
cz	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	Li	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

10

15

20

25

30

35

110 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoeitin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using secreted proteins or the genes that encode them.

10

15

20

25

30

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

10

15

20

25

30

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

PCT/US98/27059

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single-and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

5

10

15

20

25

30

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

25 Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

The translation product of this gene shares sequence homology with a neurogenic secreted signaling protein, in addition to the human UDP-galactose:2-acetamido-2-deoxy-D-glucose3beta-galactosyltransferase (See Genbank Accession No. gnllPIDle1237254) which is thought to be vital in glycoprotein biosynthesis. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: GLGPAQVALSLQGPA (SEQ ID NO:239), SSWMAGTQPRTSWWEMSS AKPCPTGTLRSNTSSHPQCTGPPTTHPMLVGEDMSCPEPQCGASRLSWKMNS

15

10

15

20

25

30

35

SPLMMSLWVCA (SEQ ID NO:240), QPRTSWWEMSSAKPCPTGTLRSN (SEQ ID NO:241), MSCPEPQCGASRLSWKMLNSSPL (SEQ ID NO:242), WVALYIEG GMKYLTLVFLLGRAWRMTSPTRRSWAGSQPSRNSNTLGTWTKTSSSPFSMK WAWGQAATTQRCRCSSLSVRLKKSSVKSHWRMSSNSLLS (SEQ ID NO:243), GGMKYLTLVFLLGRAWRMTS (SEQ ID NO:244), SQPSRNSNTLGTWTKTS SSPFSMKW (SEQ ID NO:245), and/or TTQRCRCSSLSVRLKKSSVKSHWRMS (SEQ ID NO:246). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 12. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 12.

This gene is expressed primarily in human fetal brain, epileptic frontal cortex and 12 week old early stage human.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural or immune disorders, particularly neurodegenerative conditions such as epilepsy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:125 as residues: Ala-27 to Ser-38, Pro-43 to Asn-54, Thr-115 to Asp-121, Leu-225 to Val-232, Pro-247 to Gly-252, Arg-306 to Leu-311.

The tissue distribution in fetal brain tissue, combined with the homology to a neurogenic secreted signaling protein, in addition to the conserved UDP-galactose:2-acetamido-2-deoxy-D-glucose3beta-galactosyltransferase protein indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment, detection, and/or prevention of a variety of neural disorders, particularly epilepsy and other disorders of the CNS. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are

10

15

20

25

30

not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. In addition, the protein may show utility in the creation of novel therapeutics which depend upon the localizing benefits (cell and tissue specificity) of glycoproteins. This protein may also be used to produce physiologically active saccharide chains and varients, and for improvement of saccharide chains bound to physiologically active proteins. Expression within fetal tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:11 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1257 of SEQ ID NO:11, b is an integer of 15 to 1271, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 2

10

15

20

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: ASTLAQ

TTGTCKXXXSSRRARSRTQRXFQLRPDKRSAPSLLQFIQAQEELSKENTGRQLA AREAVLALEGSTQLTGPVTQVAASKTHCSGMALTASPVPVLGAAPAKXPTO NXPGQXGRAXXKVXTSWXXVATKVLHGLEVSTHLGKRKLSGRSWLPGP ALHATPSQSHTQTGSQIVHPPQGEVREVGRGRGQPPAQPVHAHPSQQHPSPAH LAGLSLWTGTA (SEQ ID NO:247), AMLETWRPGPSXGELATNSGQRASQDSQ HSPPHVRAHLLISPLPAFPSMGGPAGRSAPXXLTETKSELQRLRRRQARASXS XPAGEPGAGHSDSFNCVPTNGQPLRSCSLSKLRRSFLKRTQGDSWLPEKQSW LWKAPPS (SEQ ID NO:248), SHQSHLINPASSAKGSWAQLKAQPPAHVLGGT GQEGPPPTADQPESPGWDPSSFTNGSSGPRALPTSVHPTLQQGAPCRRNWA PCRGLVETRMLRRQLPHGTSKRDLGWASLQRGSPQETPO (SEO ID NO:249). RPDKRSAPSLLQFIQAQEELSKENTGRQLAAREAV (SEQ ID NO:250), ATPSO SHTOTGSQIVHPPOGEVREVGRGRGOPP (SEO ID NO:251), ODSOHSPPHVR AHLLISPLPAFPSMGGPA (SEQ ID NO:252), DSFNCVPTNGQPLRSCSLS KLRRSFLKR (SEQ ID NO:253), KGSWAQLKAQPPAHVLGGTGOEGPP (SEO ID iNO 254:), KPSHQP (SEQ ID NO:256), and/or APSLLQFIQAQEELSKENTGROLA AR (SEQ ID NO:255). Polynucleotides encoding these polypeptides are also

This gene is expressed exclusively in adult human testis.

encompassed by the invention.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive disorders, particularly abnormalities of the testis, in addition 25 to impotence and infertility. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, testicular, adrogen regulated, and cancerous and wounded tissues) or 30 bodily fluids (e.g., lymph, serum, plasma, seminal fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:126 as residues: His-45 to Gly-56, Trp-62 to Tyr-68, His-94 to Trp-100.

10

15

20

The tissue distribution in testis indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention for abnormalities of the reproductive system. In addition, expression of this gene product in the testis may implicate this gene product in normal testicular function. This gene product may be useful in the treatment of male infertility, and/or could be used as a male contraceptive. Moreover, the protein product of this gene may be useful in the treatment, detection, and/or prevention of a variety of disorders related to androgen-regulated tissues, particularly the prostate gland. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:12 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1437 of SEQ ID NO:12, b is an integer of 15 to 1451, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

25 The translation product of this gene shares sequence homology with the human VAKTI precursor (See Genbank Accession No. gnllPIDle1311078 (AJ228139)), in addition to the ovoinhibitor and thrombin inhibitors, which are thought to be important in inhibition of protease activities. Contact of cells with supernatant expressing the product of this gene has been shown to increase the permeability of the plasma 30 membrane of monocytes to calcium. Thus, it is likely that the product of this gene is involved in a signal transduction pathway that is initiated when the product binds a receptor on the surface of the plasma membrane of both immunce cells, in addition to other cell-lines or tissue cell types. Thus, polynucleotides and polypeptides have uses which include, but are not limited to, activating monocytes. Binding of a ligand to a 35 receptor is known to alter intracellular levels of small molecules, such as calcium. potassium and sodium, as well as alter pH and membrane potential. Alterations in small molecule concentration can be measured to identify supernatants which bind to

receptors of a particular cell. Moreover, when tested against NIH3T3 and U937 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response) and GAS (gamma activating sequence) promoter elements. Thus, it is likely that this gene activates fibroblasts or hematopoietic cells through the EGR1 and/or JAK-STAT signal transduction pathway. EGR1 is a separate signal transduction

- JAK-STAT signal transduction pathway. EGR1 is a separate signal transduction pathway from Jak-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation. GAS is also a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal
- transduction pathway involved in the differentiation and proliferation of cells.

 Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: CSYRPQFPVDPRVRATCIVFN (SEQ ID NO:257), GTENLLA
- PERTILSRAQMGKCMATPAPCVRSSSKQKKKKRKRKVXQETKDNLRVQLPL XSCVVNXANPGKTDGFFAPERMTPSRAQMEKCMATPAPCVRPSFNKKKEQE QRLKEKLQRKSAVNFGTK (SEQ ID NO:258), LLAPERTILSRAQMGKCMAT PAPCVR (SEQ ID NO:259), PGKTDGFFAPERMTPSRAQMEKCM (SEQ ID NO:260), EQRLKEKLQRKSAVNFG (SEQ ID NO:261), KTLLENFSTQGTFVAMH
- 20 PAVRATDWITLPCTKKPSISHLFFXFLAKILFSISSNSSFTLSLGIFSFFXXQLST HCTLIAMRLPIRTKNRIIFPCASKSSISNKGPKSTAYILLWITALTFPFTFYTNL GPGFRILSTQCTSVVICFPICATNSFIIIRTDKIPISFSFFKIITIQLC WGSSLGSSC (SEQ ID NO:262), MHPAVRATDWITLPCTKKPSIS (SEQ ID NO:263), LIAMRLP IRTKNRIIFP (SEQ ID NO:264), SSISNKGPKSTAYILL WITALTFPFT (SEQ ID
- 25 NO:265), IIIRTDKIPISFSFFKIITIQLC (SEQ ID NO:266), NDGQCLAYNTTHY RERAMTSHARVSLGPSRDPLERPPFFFFFFFFFFFFFFFFFFKFEHTGTHGTLVSMHFAI WATDRIMLPGAYKCSIPHLVPKFTADFLCSFSFSLCSCSFFLLKEGLTHGAGVA MHFSIWALDGVILSGAKKPSVFPGFAXFTTQLXKGSCTL RLSFVS (SEQ ID NO:267), CLAYNTTHYRERAMTSHARVSL (SEQ ID NO:268), GTLVSMHFAI
- 30 WATDRIMLPGAYKCSIPHLVP (SEQ ID NO:269), GVILSGAKK PSVFPGFAX FTTQLX (SEQ ID NO:270), KKASHMEQVLPCIFPSGPWMGSFSLXQKSRPF FLDLRXSLHNSXKEAVLLDCLLFLXXPSFFFFSSSSAWKKTSHMEQVLPCT FPSGPWIGLFSLVQASFPFLTSFRYSLQSSAYEVAFPDSLLFLARASAFFFSSFSA WK (SEQ ID NO:271), CIFPSGPWMGSFSLXQKSRPFFLDLRXS (SEQ ID
- 35 NO:272), WIGLFSLVQASFPFLTSFRYSLQSSAYE (SEQ ID NO:273), NSAVN IKIRQRMEYFSVPEKMTLFVVQMGKCMATCVPCVKPTSKQKMKKRKRLKHE LETKENLEKQPHMQSFAVNIESL (SEQ ID NO:274). IKIRQRMEYFSVPEKMTL

10

15

20

25

30

35

FVVQM (SEQ ID NO:275), and/or VKPTSKQKMKKRKRLKHELETKENL (SEQ ID NO:276). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 5. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 5.

This gene is expressed primarily in heart, tonsils, Hodgkin's lymphoma, neuroblastoma, leukocyte and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cardiovascular, immune, or hemodynamic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., cardiovascular, muscle, immune, hematopoietic, pulmonary, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, pulmonary surfactant or sputum, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:127 as residues: Ala-20 to Gln-27.

The tissue distribution in heart and immune cells and tissues, the homology to protease inhibitors, in addition to the detected calcium flux, EGR1, and GAS biological activities indicates polynucleotides and polypeptides corresponding to this gene are useful for disgnosis and treatment of hemodynamic or vascular disorders, including hemorrhage, heart failure, and embolism, because proteases and their inhibitors are often involved in the cascades controlling hemadynamic controls. Protein may also show utility in the treatment, detection, and/or prevention of a variety of metabolic (i.e. cellular or physiological) and/or proliferative disorders in which aberrant regulation of a protease is thought to be involved, particularly in the premature activation of zymogens, for example. The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological activities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines;

10

15

20

immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating hemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behavior. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:13 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2303 of SEQ ID NO:13, b is an integer of 15 to 2317, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is greater than or equal to a + 14.

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

The translation product of this gene shares sequence homology with the ecotropic retrovirus receptor and the human cationic amino acid transporter-3 (See Genbank Accession No. gnllPIDle1198517) which are thought to be important in viral infections and amino acid and polyamine transport. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: PRVRGTVVRLRQHRPSAYILVSTVLTLMVPWHSLDPDSALADAFYQRGYRWAG FIVAAGSICA (SEQ ID NO:277), TVVRLRQHRPSAYILVSTVLTLMVP (SEQ ID NO:278), WHSLDPDSALADAFYQRGYRWAGFIV (SEQ ID NO:279), TPSCSASS SPCHALSMPWPPMGSSSRCLPMCTPGHRCLWRAPWRSGSSRPSWHCCWTWS

15

20

30

35

RWFSSCPLAHSWPTHSWPPVSLCCASRSLPRPAPQAQPALAP (SEQ ID NO:280), LSMPWPPMGSSSRCLPMCTPGHRC (SEQ ID NO:281), APWRSGSS RPSWHCCWTWSRWFSSCPL (SEQ ID NO:282), THSWPPVSLCCASRSL PRPAPQ (SEQ ID NO:283), AYILVSTVLTLMVPWHSLDPDSALADAFYQRGYRW AGFIVAAGSICAMNTVLLSLLFSLP (SEQ ID NO:284), PWHSLDPDSALADAF YQRGYRWAGFIVAAGS (SEQ ID NO:285), RIVYAMAADGLFFQVFAHVHPRTQ VPV (SEQ ID NO:286), DLESLVQFLSLGTLLA (SEQ ID NO:287), YTFVATSII VLRFQK (SEQ ID NO:288), LTKQQSSFSDHLQLVGTVHASVPEPGELKPA (SEQ ID NO:289), LRPYLGFLDGYSPGAVVTWALGVMLASAITIGCVLVFGN (SEQ ID NO:291), GAHQQQYREDLFQIPMVPLIPALSIVLNICLMLKLSYLTWVRFSIW LLMGLAV (SEQ ID NO:292), MVPLIPALSIVLNICLMLKLSYLTWV (SEQ ID NO:293), and/or YFGYGIRHSKENQRELPGLNSTHYVVFPR (SEQ ID NO:294). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in placenta and brain tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive, neural, or metabolic disorders, in addition to viral infections. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system and placenta, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, neural, hepatic, metabolic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, bile, amniotic fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:128 as residues: Gln-87 to Ser-99, Pro-102 to Phe-110, Gln-204 to Leu-211, Ser-262 to Glu-268, Pro-294 to His-305.

The tissue distribution in placenta, combined with the homology to a retroviral receptor and cationic amino acid transporters, indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and intervention of viral infections, or diseases and malfunctions related to amino acid transport.

Specifically, soluble forms of this protein or, polynucleotides of the present invention.

10

15

20

can be used to bind to retroviruses so as to prevent their entry and infection of susceptible cells. They can be used for therapy/prevention of HIV infection and certain forms of leukaemia. Polynucleotide or polypeptides of the present invention can be used to identify susceptibility to retroviral infection. Based upon the tissue distribution in the brain, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:14 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1458 of SEQ ID NO:14, b is an integer of 15 to 1472, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where b is greater than or equal to a + 14.

30

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 5

In specific embodiments, polypeptides of the invention comprise the following
amino acid sequence: FPPSPAPPHSLPLRSWLWSRQMG (SEQ ID NO:295), GTSF
RGMISTQPGSTPLASFKILALESADGHGGCSAGNDIGPYGERDDQQVFIQKVVP
SASQLFVRLSSTGQRVCSVRSVDGSPTTAFTVLECEGSPAARLSAPALPAHWP

10

15

20

30

35

GQRQLGHVGPNHRHGRPRPGPCRWPDGAR ADGTAGTL (SEQ ID NO:296), PGSTPLASFKILALESADGHGGCSAGNDI (SEQ ID NO:297), GERDDQQVF IQKVVPSASQLFVRL (SEQ ID NO:298), RSVDGSPTTAFTVLECEGSPAARLS (SEQ ID NO:299), PALPAHWPGQRQLGHVGPNHRHGRPR (SEQ ID NO:300), PFIPRRPWPEPGVPTGIREAPESPRTRASQGIMAAALFKKEVSLSFILGGVRG VPRPLEGHGAGVGGRRRSGPLRTSSWQRSTKLPPPRRRASACGGLGLPRWP DKEVLLEAEWRLVREMRGEGLGRQPHEGAERSRRGQLTVFQLFHQLLLRQATC RGLA EAVHGGG (SEQ ID NO:301), PGVPTGIREAPESPRTRASQGIMAAALF KKEV (SEQ ID NO:302), FILGGVRGVPRPLEGHGAGVGGRRRSGP (SEQ ID NO:303), GLPRWPDKEVLLEAEWRLVREMRG (SEQ ID NO:304), and/or GAER SRRGQLTVFQLFHQLLLRQ (SEQ ID NO:305). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in human fetal kidney, and to a lesser extent, in thymus and bone marrow cell line (RS4;11).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental, metabolic, immune or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., developmental, metabolic, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.,

25. lymph, serum, amniotic fluid, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:129 as residues: Thr-17 to Trp-26, Pro-54 to Trp-61, Ala-65 to Arg-74, Pro-142 to Leu-147, Pro-158 to Ala-165.

The tissue distribution in thymus and bone marrow cell lines indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of immune disorders involving stem cells. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are

10

15

20

25

30

important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, the expression within fetal kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilm's Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Moreover, the expression within fetal tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:15 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1002 of SEQ ID NO:15, b is an integer of 15 to 1016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 6

35

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: HASAHASAHASGCGA (SEQ ID NO:306), QGVGVADEGG

LERQRVDAGARLGHMGQPVAFSTRQLHLALPAPGTAGVTVPHPHAREGVV GDLPLVPDAEDPTVGVPAEGLLVLGHVVERAELILVRGLHQAEALARESEEMH GSRHG (SEQ ID NO:307), EGGLERQRVDAGARLGHMGQPVAFS (SEQ ID NO:308), LALPAPGTAGVTVPHPHAREGVVGDLPLV (SEQ ID NO:309), PAEG

- 5 LLVLGHVVERAELILVRGLHQAEA (SEQ ID NO:310), HLFKFFYTIAFMQWF TEFMELFLSVWELIKTXNLCFVCFSEHKPGQLVPAGPTSQLLCRALGRVH LCSPTTRSQTPTQSWVTPQLLWRLGSGRLVAQVLQVGSFCGPRVGDAVLGEQT FQP FDLL (SEQ ID NO:311), AFMQWFTEFMELFLSVWELIKTXNLCFVC (SEQ ID NO:312), and/or RSQTPTQSWVTPQLLWRLGSGRLVAQ (SEQ ID NO:313).
- Polynucleotides encoding these polypeptides are also encompassed by the invention.

 The gene encoding the disclosed cDNA is believed to reside on chromosome 16.

 Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 16.

This gene is expressed primarily in human infant brain, and to a lesser extent, in adult brain and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural, developmental, or pulmonary disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system (CNS), expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, developmental, pulmonary, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, amniotic fluid, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:130 as residues: Ser-47 to Pro-57, Ser-77 to Glu-82, Thr-90 to Trp-98, Arg-124 to Lys-137, Ala-183 to Glu-192, Lys-220 to Gln-229, Asn-244 to Arg-258, Thr-271 to Asn-278, Glu-285 to Gly-297.

The tissue distribution in infant and adult brain indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of diseases of the CNS, such as mental retardation, schizophrenia, Alzheimer's disease, paranoia, depression, and mania. Moreover, polynucleotides and

15

20

10

15

20

25

30

polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, dementia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. The protein product of this gene may also show utility in the detection, treatment, and/or prevention of a variety of pulmonary disorders, particularly those related to disorders of the mucosal or endothelial tissues. The expression within fetal tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:16 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1225 of SEQ ID NO:16, b is an integer of 15 to 1239, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to a + 14.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

10

15

20

25

30

The gene encoding the disclosed cDNA is believed to reside on chromosome 17. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 17. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: GAWGVEVVAVGSKAGCLVYQLCDLKQITFFFRASVCLSV (SEQ ID NO:314), PASLGSSWGQKLRGGTRKSFQELSPSSAPPACLPQPPASTWLSSWPRPPCW PPMCSWALGXCFCPATGQWLPTSCCLWWCPDAGGRQKHFRSRWXTSWETW QPYLTGLISSVLRAXRPDSYLQRFRSLXQXXLCCAFVIALGGGCFLLTALYLER DETRAWQXVTGTPDSNDVDSNDLERQGLLSGXGASTEEP (SEQ ID NO:315), L RGGTRKSFQELSPSSAPPACLPQPP (SEQ ID NO:316), ATGQWLPTSCCLW WCPDAGGRQKHFRSR (SEQ ID NO:317), GGCFLLTALYLERDETRAWQXV (SEQ ID NO:318), APHLRLQPACHSPLPLPGSRPGPDHPAGLLCVPGPWGX ASVLQLGSGCRHPAVCGGAQMPGDGRSTSDHGGXHPGXPGSPISQDLSLVSC GPXALTPICSASAAXXXXXCAAPLSSPWGAAASC (SEQ ID NO:319), PACHSPLPLPGSRPGPDH PAGLLCV (SEQ ID NO:320), and/or SGCRHPAVCGGAQMPGDGRSTSDHGG (SEQ ID NO:321). Polynucleotides

This gene is expressed primarily in pineal gland and thymus.

encoding these polypeptides are also encompassed by the invention.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune, endocrine, emotional or behavior disorders, in addition to autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, endocrine, hematopoietic, neural, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:131 as residues: Asp-18 to Gln-27, Arg-44 to Asn-49.

The tissue distribution in thymus indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of

immune and autoimmune diseases, such as lupus, neutropenia, transplant rejection, and inflammatory diseases. Moreover, the expression within pincal gland indicates the protein product of this gene may be useful in disorders associated with biological clock aberrations, emotional distress, lethargy, or metabolic conditions. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:17 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1391 of SEQ ID NO:17, b is an integer of 15 to 1405, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

20

25

30

35

15

5

10

When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon-sensitive responsive element) promoter element. Thus, it is likely that this gene activates leukemia cells, or more generally, immune or hematopoietic cells, through the JAK-STAT signal transduction pathway. ISRE is a a promoter element found upstream in many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: ${\tt GLKVMEICSLTFLEATNLQSRCQQAMLPLKALRKNPFLLLPSFDGCCQSLA}$ FPGLWLQHSNLCLNHHMTFLVYLLCVSVFKYFFPFSCTYTSHWI (SEQ ID NO:322), ICSLTFLEATNLQSRCQQAMLP (SEQ ID NO:323), and/or GLWLQHS NLCLNHHMTFLVYLLCVSV (SEQ ID NO:324). Polynucleotides encoding these polypeptides are also encompassed by the invention.

10

15

20

25

30

35

This gene is expressed primarily in IL-1 and LPS induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, particularly inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:132 as residues: Ser-45 to His-50, His-52 to Ile-57, Lys-67 to His-81.

The tissue distribution in neutrophils, combined with the detected ISRE biological activity indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of inflammatory disorders, such as psoriasis, inflammatory bowel disease, rheumatoid arthritis, and sepsis. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:18 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

20

25

30

35

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1520 of SEQ ID NO:18, b is an integer of 15 to 1534, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: PFPLLPPKRRGLLYHLIQKSTLGLVVWFREHLDSRSQ (SEQ ID NO:325), RGXPSWPMHTLVYAQHSTTHTPLIQPQWTQVIDQPPGITHQFCVR XCXCPTLESCVQECVTRSRXKPTTGVPGPQRLA (SEQ ID NO:326), TPLIQPQW TQVIDQPPGITHQFCV (SEQ ID NO:327), ALGPSQTCDLDVWLVAKPSFFRGPQ GIHYFSLWRRKPLSHWVSIWQLQGQETMPAMLRSRPAGQATVATGPPRGSPS PQDLPSYHRKQVESSHRHSWEPASQSQ (SEQ ID NO:328), CDLDVWLVAKPSF FRGPQGIHYFSLWRR (SEQ ID NO:329), and/or AGQATVATGPPRGSPSPQDLP SYHRKQV (SEQ ID NO:330). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in synovial fibroblasts, and to a lesser extent, in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, skeletal or vascular disorders, particularly arthritis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.,skeletal, vascular, endothelial, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in synovial fibroblasts indicates polynucleotides and polypeptides corresponding to this gene are useful for treatment of arthritis. Moreover, polynucleotides and polypeptides corresponding to this gene are useful in the detection

and treatment of disorders and conditions afflicting the skeletal system, in particular osteoporosis, bone cancer, as well as, disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (i.e. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). The protein product of this gene may also be useful for the detection, treatment, and/or prevention of a variety of vascular disorders which include, but are not limited to, atherosclerosis, embolism, stroke, microvascular disease, or aneurysm. The protein may also be useful in the treatment of integumentary disorders, particularly those related to aberrations in the extracellular matrix or lamina. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:19 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1219 of SEQ ID NO:19, b is an integer of 15

to 1233, where both a and b correspond to the positions of nucleotide residues shown

25

20

5

10

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

in SEQ ID NO:19, and where b is greater than or equal to a + 14.

In specific embodiments, polypeptides of the invention comprise the following

amino acid sequence:

XGDTXTQNSRHDTPXLIDYYRESCTLQYRPEFPGRPTRPRGSCPQYPGPAIPRT

SWALGEGDAAPRGAHH PRRADVPLG (SEQ ID NO:331), YRESCTLQYRPEFPG

RPTRPRGSCPQYPGP (SEQ ID NO:332), GKLYAAVPSGIPGSTHASARLMPPVS

RSSYSEDIVGSRRRRSSSGSPPSPQSRCSSWDGCSRSHSRGREGXRPPWSEL

DVGALYPFSRSGSRGRLPRFRNYAFASSWSTSYSGYRYHRALLCRRTAVSGR

LREGREPSAEEAEGEREDWGIGSA (SEQ ID NO:333), SGIPGSTHASARLMPP

10

15

20

25

30

VSRSSYS (SEQ ID NO:334), GCSRSHSRGREGXRPPWSELDVGALYPFS (SEQ ID NO:335), TAVSGRLREGREPSAEEAEGEREDW (SEQ ID NO:336), RIRKAA VQIPTRKNIGXRRPVVQETRKKERISRLKESĮGNILIVTVTQSLTQILTLMMI KRELKPRKRRKRNTKQXKRRIRKPKKNPVTQAVKTQKRTCQKLPGMEQ PNVADTMDLIGPEAPINTYLFKMKNL (SEQ ID NO:337), TRKKERISRLKESI GNILIVTVTQSLTQ (SEQ ID NO:338), and/or VKTQKRTCQKLPGMEQPNVA DTMDLIGP (SEQ ID NO:339). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 6. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 6.

This gene is expressed primarily in retina.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, visual disorders, particularly retinopathy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the ocular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, vitreous humor, aqueous humor, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in retina indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of diseases of the retina, for example, diabetic retinopathy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:20 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1076 of SEQ ID NO:20, b is an integer of 15

to 1090, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.

5

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

When tested against NIH3T3 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) promoter element. Thus, it is likely that this gene activates fibroblast cells, or more generally, other cells of the integumentary system, through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jak-STAT. Genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

LPFTLKPKMVKIPFSSRLINNNLQYIDCILSLKRCEEILLMWHGLLLCLASVFLE LRGDRPPLLASLLEPHKMPLHSSSL (SEQ ID NO:340), LKPKMVKIPFSSRLIN NNLQYIDC (SEQ ID NO:341), SLKRCEEILLMWHGLLLCLASVF (SEQ ID NO:342), LRGDRPPLLASLLEPHKMPLH (SEQ ID NO:343), LQMHTGSGFKGK SCEVAFYVAQAEKPGEGAYLHGAQETQKQGIEADHATLRGSPHSVSKTKYNLY IANYYLLAWRKMES (SEQ ID NO:344), CEVAFYVAQAEKPGEGAYLH (SEQ ID

Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in human ovarian cancer.

NO:345), and/or ATLRGSPHSVSKTKYNLYIANYY (SEQ ID NO:346).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive disorders, particularly cancers, such as ovarian cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the female reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the

10

15

20

30

expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in human ovarian cancer tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of ovarian cancer. Moreover, the expression within cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:21 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 668 of SEQ ID NO:21, b is an integer of 15 to 682, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 12

Contact of cells with supernatant expressing the product of this gene increases the permeability of the plasma membrane of myeloid leukemia cells to calcium. Thus, it is likely that the product of this gene is involved in a signal transduction pathway that is initiated when the product binds a receptor on the surface of immune or hematopoietic cells, in addition to other cells or cell types. Thus, polynucleotides and polypeptides have uses which include, but are not limited to, activating myeloid cells. Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium and sodium, as well as alter pH and membrane potential.

Alterations in small molecule concentration can be measured to identify supernatants which bind to receptors of a particular cell. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

15

20

25

30

35

LSASLLDRYPASESNNYIFNFVLYMLHFLAGTLFSLFPDFELSPRSATLFPDLR TVQLLSSRPHL (SEQ ID NO:347), LLDRYPASESNNYIFNFVLYMLH (SEQ ID NO:348), FPDFELSPRSATLFPDLRTV (SEQ ID NO:349), NGGFYDVSFKQAG LIEFLCIIYFYPMAHVICGSRFTIVRTIPVHYVGEYFIKSSIWILYRINERTATKK AASDFQKNFRCFLDAF (SEQ ID NO:350), KQAGLIEFLCIIYFYPMAH (SEQ ID NO:351), and/or YFIKSSIWILYRINERTATKKAA (SEQ ID NO:352). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, particularly immunodeficiencies and inflammatory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in anergic T-cells, combined with the detected calcium flux biological activity, indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders, particularly those involving anergic T-cells. Moreover, the secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, and as nutritional supplements. It may also have a very wide range of biological acitivities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac

infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:22 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 756 of SEQ ID NO:22, b is an integer of 15 to 770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

20

25

30

35

5

10

15

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: SPRXGRXFXTSRKQISGFLEFD (SEQ ID NO:353). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, particularly leukemia or multiple myeloma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the

10

15

20

25

expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in bone marrow tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of some types of leukemia, and other disorders involving bone marrow tissues or cells. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:23 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 551 of SEQ ID NO:23, b is an integer of 15 to 565, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to a + 14.

30 FEATURES OF PROTEIN ENCODED BY GENE NO: 14

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: MKHAAFGLIPLVKEIYRYLKIKSKLLIGSGKCQLQPEWL QTSLINSSLLMDWLTPY (SEQ ID NO:354), IYRYLKIKSKLLIGSGKCQLQPE WLQTSL (SEQ ID NO:355), QLGLPWDQSKGPRKNGLSMCGSVYSTIWSLIA SRREETIRVIVLYIQSPNINTRHISKRGLNKALTNP (SEQ ID NO:356), SKGPR

10

15

20

25

30

KNGLSMCGSVYSTIWS (SEQ ID NO:357), and/or QSPNINTRHISKRGLNK (SEQ ID NO:358). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in adult retina, and to a lesser extent, in 12 week old early stage human.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, visual or developmental disorders, particularly retinopathy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the ocular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., visual, developmental cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, amniotic fluid, aqueous humor, vitreous humor, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in human retina indicates polynucleotides and polypeptides corresponding to this gene are useful for treatment of retinopathy, and other disorders involving the visual system. Moreover, the expression within embryonic tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:24 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1342 of SEQ ID NO:24, b is an integer of 15

15

20

25

30

35

to 1356, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 15

The translation product of this gene has homology to the conserved human non-differentiated blood cell tyrosine kinase receptor fragment (See Genbank Accession No. R76466) which is thought to be important in signalling essential cellular pathways. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: HPQTSAGGFPLHQGLPTVS (SEQ ID NO:359), PSWFPELSPWPLKTL KKRRQMRLRRRGRLCRLSPATTTTADTCRCPARSYRGSGRRPACAQDSPAPPS RPTRRAWEKCALRPKRAAQWSTGVPPSPRSSTTGCCFGTAAXCAEGARR (SEQ ID NO:360), TTTADTCRCPARSYRGSGRRPA (SEQ ID NO:361), and/or PSRPTRRAWEKCALRPKRAAQWST (SEQ ID NO:362). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in human fetal epithelium.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental, integumentary, immune, or hematopoietic disorders, particularly skin cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the integumental system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., developmental, integumentary, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, amniotic fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:139 as residues: Gln-26 to Ala-39, Cys-48 to His-55.

The tissue distribution in human fetal epithelium, combined with the homology to a conserved tyrosine kinase receptor, indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of skin cancer, or other disorders related to the integument, particularly proliferative

10

15

20

25

conditions. Similarly, polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e. wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. In addition, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils. cellulitis, erysipelas, impetigo, tinea, althletes foot, and ringworm). Moreover, the protein product of this gene may also be useful for the treatment or diagnosis of various connective tissue disorders such as arthritis, trauma, tendonitis, chrondomalacia and inflammation, autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma. and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:25 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 603 of SEQ ID NO:25, b is an integer of 15 to 617, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 16

15

20

25

30

35

When tested against PC12 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) pathway. Thus, it is likely that this gene activates sensory neuron cells, or generally other cells or cell types, particularly immune cells, through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jak-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

ARGVLNLRNRFECFSIIETV (SEQ ID NO:363), IGQLVMKSICHFQRLLSVAI DFASQFLKNYIFSSTHSSKAGFSVVCSLPKWLYTDGMEMVLKITHKLSF (SEQ ID NO:364), and/or QRLLSVAIDFASQFLKNYIFSSTH (SEQ ID NO:365).

DFASQFLKNYIFSSTHSSKAGFSVVCSLPKWLYTDGMEMVLKITHKLSF (SEQ ID NO:364), and/or QRLLSVAIDFASQFLKNYIFSSTH (SEQ ID NO:365). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 8. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 8.

This gene is expressed primarily in fetal liver, and to a lesser extent, in resting T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune, hematopoietic, or hepatic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic, hepatic, metabolic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, amniotic fluid, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in fetal liver and resting T-cells, combined with the detected EGR1 biological activity indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of immune disorders involving T-cells, and more generally, hematopoietic conditions. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia,

-- 10

15

pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Additionally, expression within fetal tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:26 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 634 of SEQ ID NO:26, b is an integer of 15 to 648, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 17

30

35

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: LMKTASRMLLLE (SEQ ID NO:366). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in CD34-positive T cells from cord blood, and to a lesser extent, in anergic T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, particularly in immune system maturation and hematopoeitic development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, amniotic fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:141 as residues: Ile-46 to Tyr-56.

15 The tissue distribution in CD34-positive T cells and anergic T cells. indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of diseases involving nematopoeitc development and stem cell maturation, including protection of stem cells from chemotherapy, immunosuppression during transplant rejection, and neutropenia. Moreover, this gene product may be involved in the regulation of cytokine production, 20 antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, 25 rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versusgraft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune 30 infertility, lense tissue injury, demyelination, systemic lupus erythematosis, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy 35 targets for the above listed tissues.

5

10

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:27 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1374 of SEQ ID NO:27, b is an integer of 15 to 1388, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

When tested against U937 and Jurket cell lines, supernatants removed from 15 cells containing this gene activated the GAS (gamma activating sequence) pathway. Thus, it is likely that this gene activates myeloid and T-cells, or more generally cells of immune or hematopoietic origin, through the JAK-STAT signal transduction pathway. GAS is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway 20 involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: ATXWDXPGCRNSARGERLHVGDAPW (SEQ ID NO:367), ARDER 25 REVLKTLMRLSTQRPQAFLPSQSWFVRLQKAGEGALKQENSLTIQNCLLCL PRVHRQRPTPPQPQRGNTEASVLQTSTEHLPRAAVLLVPNSCSPGXPTXLLSS (SEQ ID NO:368), ERREVLKTLMRLSTQRPQAFLP (SEQ ID NO:369), GALKQEN SLTIQNCLLCLPRVHRQR (SEQ ID NO:370), and/or SVLQTSTEHLPRAAVLLVP NS (SEQ ID NO:371). Polynucleotides encoding these polypeptides are also 30 encompassed by the invention.

This gene is expressed primarily in activated human neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, such as neutropenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

15

20

25

30

35

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:142 as residues: Val-25 to Gly-33.

The tissue distribution in activated neutrophils, combined with the detected GAS biological activity, indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of immune disorders involving neutrophils. Moreover, this gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosis, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:28 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of

a-b, where a is any integer between 1 to 602 of SEQ ID NO:28, b is an integer of 15 to 616, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where b is greater than or equal to a + 14.

5

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 19

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: ALVISNPLL (SEQ ID NO:372), PYINTQMCVSSRNKFCISG HQKYDSHGRETRFEMHKARASSWKNILKIRSLKIISRGFEITNA (SEQ ID NO:373), KFCISGHQKYDSHGRETRFEMHKARAS (SEQ ID NO:374), HTLLEI ANPLQAAVLGASSIHPSIHTSTHLMFMGLKWTELHHSPDSVQGAGAAEAAQTR HSLRPGRGRERHDCTLKNLTLFIIC (SEQ ID NO:375), NPLQAAVLGASSIHP SIHTSTH (SEQ ID NO:376), and/or SLRPGRGRERHDCTLKN (SEQ ID NO:377). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, such as neutropenia, inflammatory, or allergic conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in neutrophils indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of immune disorders involving neutrophils, or more generally, immune or hematopoietic disorders. Moreover, the expression of this gene product indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other

10

15

20

25

processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia,

granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosis, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:29 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 814 of SEQ ID NO:29, b is an integer of 15 to 828, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

This gene is expressed primarily in 7 week old early stage human.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, fetal or developmental abnormalities, particularly congenital defects, including metabolic conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,

10

15

20

25

30

particularly of the developmental systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., developmental, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, amniotic fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in 7 week old early stage human tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of fetal abnormalities. Expression within embryonic tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Futhermore, the protein is useful in the diagnosis, prevention, and/or treatment of various metabolic disorders such as Tay-Sachs disease, phenylkenonuria, galactosemia, hyperlipidemias, porphyrias, leukemias, or Hurler's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:30 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 567 of SEQ ID NO:30, b is an integer of 15 to 581, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

AENVHCTPAWETGRDSEDGKGREGMGRDRKGWDGTGLDGTGWEGKRERNV

15

20

25

30

35

PA (SEQ ID NO:378), GRDSEDGKGREGMGRDRKGWDGTGLD (SEQ ID NO:379), TSLGDLWDYNNSSH (SEQ ID NO:380), DRRIIRTREAAVAVSRERP LHSSLGNRERLRRWEGTGRDGKGQEGMGRDGTGWDGMGREERKKCPS (SEQ ID NO:381), RPLHSSLGNRERLRRWEGTGRDGKG (SEQ ID NO:382), NQSWGPMGL (SEQ ID NO:383), GGGGCSEPRTSIALQPGKQGETPKMGRD GKGWEGTGRDGTGRDWMGRDGKGREKEMSQQ (SEQ ID NO:384), KQGE

TPKMGRDGKGWEGTGRDWMGRDGKGREKEMSQQ (SEQ ID NO:384), KQGE TPKMGRDGKGWEGTGRDGTG (SEQ ID NO:385), and/or PVLGTYGTITTPV TELTKGQEKEGGVETVLYE (SEQ ID NO:386). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in frontal cortex from a patient suffering from schizophrenia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural disorders, such as Schizophrenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in frontal cortex tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of some central nervous system disorders, for example, schizophrenia. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioural disorders, or inflamatory conditions such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural

15

25

30

35

function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Moreover, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:31 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 775 of SEQ ID NO:31, b is an integer of 15 to 789, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to a + 14.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 22

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: KIVFIDQKWSK (SEQ ID NO:387), CSLFWGILFLSRLRIH LFLSLKPCMCLRPIDILSHFLDIFVTSVLSELEKSSLKTTETFSFAVFLLLMMN (SEQ ID NO:388), LSRLRIHLFLSLKPCMCLRPIDILSH (SEQ ID NO:389), and/or VLSELEKSSLKTTETFSFAVFL (SEQ ID NO:390). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in thymus and neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, particularly inflammation, or disorders related to immune cell maturation and/or activation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain

tissues or cell types (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:146 as residues: Lys-38 to Leu-46.

The tissue distribution in thymus and neutrophils indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of inflammatory disorders, such as psoriasis, inflammatory bowel disease, rheumatoid arthritis, and sepsis. Moreover, the expression of this gene product indicates a role in regulating the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versushost diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosis, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:32 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 870 of SEQ ID NO:32, b is an integer of 15 to

5

10

15

20

25

15

20

884, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 23

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: TLFRYILH (SEQ ID NO:391). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases and disorders afflicting blood cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoeitic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:147 as residues: Pro-30 to Asn-36.

The tissue distribution in bone marrow indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of diseases afflicting the blood, including leukemia, neutropenia, anemia, and stem cell protection during chemotherapy. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the

expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:33 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

10 polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 852 of SEQ ID NO:33, b is an integer of 15 to 866, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to a + 14.

15

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

This gene is expressed primarily in Merkel cells.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, integumentary disorders, particularly aberrations in mechanic sensory function. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) 25 or cell type(s). For a number of disorders of the above tissues or cells, particularly in tissues involved in sensory function, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., integumentary, sensory, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell 30 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in Merkel cells indicates polynucleotides and polypeptides corresponding to this gene are useful for Merkel cell dysfunctions, which 35 may include aberrations in sensory function. Alternatively, polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or

WO 99/31117

prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma),

injuries and inflammation of the skin (i.e. wounds, rashes, prickly heat disorder, 5 psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. In addition, such disorders may predispose increased susceptibility to

viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum 10 contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, althletes foot, and ringworm). Moreover, the protein product of this gene may also be useful for the treatment or diagnosis of various connective tissue disorders such as arthritis, trauma, tendonitis, chrondomalacia and inflammation, autoimmune disorders such as

rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, 15 spinal deformation, and specific joint abnormalities as well as chondrodysplasias (i.e. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets 20 for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:34 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. 25 Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:34, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

35 The translation product of this gene shares sequence homology with dihydropyridine receptor or nitrate transporter which are thought to be important in transport of small molecules across the cell membrane. In specific embodiments,

10

15

20

25

30

35

polypeptides of the invention comprise the following amino acid sequence: GTSFSVLSLIHDTG (SEQ ID NO:392). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 11. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 11.

This gene is expressed primarily in kidney cortex and muscle tissue from a patient with multiple sclerosis, and to a lesser extent, in fetal liver/spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, muscle, urogenital, or renal disorders, particularly musculodegenrative conditions such as multiple sclerosis, in addition to kidney or metabolic disorders and diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the multiple sclerosis and renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., muscle, urogenital, renal, hepatic, metabolic, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, bile, amniotic fluid, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:149 as residues: Ala-66 to Leu-73.

The tissue distribution in kidney cortex and muscle tissue, combined with the homology to small molecule transporters indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of disorders of renal functions and muscular diseases, including multiple sclerosis, muscular dystrophy, cardiomyopathy, fibroids, myomas, and rhabdomyosarcomas. The tissue distribution in kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilm's Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor

10

15

20

marker and/or immunotherapy targets for the above listed tissues. The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological activities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating hemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behavior. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. .

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:35 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1201 of SEQ ID NO:35, b is an integer of 15 to 1215, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to a + 14.

30

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

35 VLISASTIGSRTSGAQGMEKMTIPTLAVGEPKTPEKSKCSLKQCFSSCNVHIDH LGLLLKCKF (SEQ ID NO:393), ASTIGSRTSGAQGMEKMTIPTLA (SEQ ID

10

15

20

25

30

35

NO:394), and/or GEPKTPEKSKCSLKQCFSSCNVHIDHL (SEQ ID NO:395). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in kidney medulla.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, renal, urogenital, or more generally, disorders afflicting endothelial tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., renal, urogentital, endothelial, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in kidney medulla indicates polynucleotides and polypeptides corresponding to this gene are useful for the disgnosis, treatment, and/or prevention of renal disorders, including lesions, vascular diseases, hydronephrosis, and renal diseases associated with systemic disorders. Moreover, the gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilm's Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. The protein product can also be used for the treatment, detection, and/or prevention of various endothelial disorders, which include microvascular disease, embolism, aneurysm, stroke, or atherosclerosis. Protein, as well as, antibodies directed against the protein may show utility as a tumor

marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:36 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1780 of SEQ ID NO:36, b is an integer of 15 to 1794, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.

5

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

RIRSQDLAIMTTCFKKYEFSFFVLGFLRRWGATLCLGFTSFAIKFHPSSLCSEKE GKDFSGFALSIHGPERKKEEGWARWLTPVVPVLWEAEVGGSPEVSS (SEQ ID NO:396), TTCFKKYEFSFFVLGFLRRWGA (SEQ ID NO:397), SEKEGKDFSGF ALSIHGPERKKEEGW (SEQ ID NO:398), MNECIAKPCMAAFCSCPSCCLPSR PGCSREQRCAFSCEPCHTVEHWVEPMGQGQRQEHTQGSVLPSSHPSRGKATT VHSCCQEPWG (SEQ ID NO:399), FCSCPSCCLPSRPGCSREQRCAFSCEP (SEQ ID NO:400), GQRQEHTQGSVLPSSHPSRGKAT (SEQ ID NO:401), GVVNSCLL PLPPRLLATGMDCGGFASRRMGGRQHAALSVFLPLPLAHGLYPMFNCVAGLT GKGTSLLSGAARPAGEAAARAGTKGSHARFGNAFIHSF HSFIECLLNTYCVP

SSALTAVGIGDILKNKNDKSSCLCSC (SEQ ID NO:402), GMDCGGFASRRMG GRQHAALSVFLP (SEQ ID NO:403), LTGKGTSLLSGAARPAGEAAARAGT (SEQ ID NO:404), and/or LNTYCVPSSALTAVGIGDILKN (SEQ ID NO:405).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, pulmonary or developmental disorders and/or diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., pulmonary, developmental, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, pulmonary surfactant or sputum, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression

10

15

20

30

35

level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in fetal lung indicates polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of diseases related to pulmonary functions and infections. Moreover, the expression within fetal tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:37 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1160 of SEQ ID NO:37, b is an integer of 15 to 1174, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 28

This gene is expressed primarily in hepatocellular tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, metabolic or hepatic disorders or diseases, particularly hepatocellular tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., metabolic, hepatic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, bile, plasma, urine, synovial fluid and

10

15

20

spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in hepatocellular tumors indicates polynucleotides and polypeptides corresponding to this gene are useful for disgnosis and treatment of hepatic disorders, particularly proliferative conditions such as hepatocellular tumors. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In addition, the protein may play a role in the treatment, detection, and/or prevention of developmental abnormalities, fetal deficiencies, pre-natal disorders and various would-healing models and/or tissue trauma. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:38 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1073 of SEQ ID NO:38, b is an integer of 15 to 1087, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:38, and where b is greater than or equal to a + 14.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

The translation product of this gene has homology to a contains a helix-loop30 helix motif from a Caenorhabditis elegans protein (See Genbank Accession No.
gil1326280) which is thought to function as a modulator of gene expression. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

TSLSQLWHFCHFWPVKFCCGGCPVHCRMFSSISGLYLLNASAPSLQLNDPKCL

QT (SEQ ID NO:406), and/or WPVKFCCGGCPVHCRMFSSISGLYLLNA (SEQ ID NO:407). Polynucleotides encoding these polypeptides are also encompassed by the invention.

10

15

20

25

30

This gene is expressed primarily in normal breast.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive, or endocrine disorders, particularly of the breast, such as breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer and metabolic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, endocrine, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, breast milk, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in breast indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of some types of breast cancer. The protein can also be used for the treatment, detection, and/or prevention of disorders related to ductile tissues or cell types, particularly secretory dysfunctions. The protein can also be used for the treatment of vascular disorders such as atherosclerosis, microvascular disease, embolism, stroke, or aneurysm. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:39 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 424 of SEQ ID NO:39, b is an integer of 15 to 438, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

10

15

20

25

30

35

When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon-sensitive responsive element) promoter element. Thus, it is likely that this gene activates leukemia cells, or potentially other cells or cell-types, through the JAK-STAT signal transduction pathway. ISRE is a promoter element found upstream in many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

SCRCWALGAGGGQRQWVGRS (SEQ ID NO:408), TGAQAPKMGARQRKRPL QTRIKNSSKSTLWPPQWVRCGRWWTWPSRKKTSRPRRQLFTSTLSTSASALV WPVSWFSQEGH (SEQ ID NO:409), MGARQRKRPLQTRIKNSSKSTLWPP (SEQ ID NO:410), and/or PRRQLFTSTLSTSASALVWPVSW (SEQ ID NO:411).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in human testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive disorders, particularly abnormalities of the testes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, testicular, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, seminal fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:154 as residues: Leu-26 to Glu-52, Gln-71 to Lys-79.

The tissue distribution in testes, combined with the detected ISRE biological activity, indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of abnormalities of the testes, such as male infertility and proliferative conditions, and/or could be used as a male

contraceptive. The protein can also be used for the maintainance normal testicular function. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:40 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 720 of SEQ ID NO:40, b is an integer of 15 to 734, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where b is greater than or equal to a + 14.

15

20

25

30

35

10

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 31

This gene is expressed primarily in colon, and to a lesser extent, in thymus. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, gastrointestinal, immune, or hematopoietic disorders, particularly abnormalities of the colon, and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., gastrointestinal, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in colon and thymus tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of abnormalities of the colon. The protein can also be used for treating inflammatory conditions, or potentially in modulating immune system activation in the treatment of gastrointestinal disorders. Protein, as well as, antibodies directed against

the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:41 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1332 of SEQ ID NO:41, b is an integer of 15 to 1346, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 32

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: DGGGKEEGVSCLKISLLCGPWLWLP (SEQ ID NO:412), HE MGELAICHTRVPFSLPSSAQGVPQNLQGPIGHLAVCTPSSLTSWHFPQKREKW STVNKRQRFLQFPAPLRNWIPQTPLSLSVSSGPLGSFTVFTLLSLCAWPWCCRD 20 CYKSCCPIPIFNLTAPLCVHTPEPSS (SEQ ID NO:413), SSAQGVPQNLQGPIGH LAVCTPS (SEQ ID NO:414), VNKRQRFLQFPAPLRNWIPQTPLSLSVS (SEQ ID NO:415), CCRDCYKSCCPIPI FNLTAPLCV (SEQ ID NO:416), DLNVTNEGEGKE VLGQGSTNNEKKCQKATSNTEPRAREAKARHANMGTSDRESPTWSLTAE GLKAKSKMQGKATKGAASTMGSHNQGPHKREIFKHETPSSFPPPSQCQPE 25 LLPYKYWATLASGYVPSWLPSVDSYRINTAIKDKNGQDT (SEQ ID NO:417), VLGQGSTNNEKKCQKA TSNTEPRA (SEQ ID NO:418), RESPTWSLTAE GLKAKSKMQGKATKGAAS (SEQ ID NO:419), and/or GYVPSWLPSVDSYRI NTAIKDK (SEQ ID NO:420). Polynucleotides encoding these polypeptides are also 30 encompassed by the invention.

This gene is expressed primarily in rhabdomyosarcoma, and to a lesser extent in heart and thymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, muscle disorders, particularly rhabdomyosarcoma and other proliferative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are

useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., muscle, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:156 as residues: Gly-28 to Asp-33.

The tissue distribution in rhabdomyosarcoma tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of rhabdomyosarcoma. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various muscle disorders, such as muscular dystrophy, cardiomyopathy, fibroids, or myomas. The protein can also be used for the amelioration of proliferative conditions in other tissues, including modulation of the immune respone to such tissues. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:42 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 984 of SEQ ID NO:42, b is an integer of 15 to 998, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where b is greater than or equal to a + 14.

30

10

15

20

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 33

In specific embodiments, polypeptides of the invention comprise the following
amino acid sequence: NSAEQSMLILVT (SEQ ID NO:421), RXDRXPVPELPGYEPT
RTDISSFKNIYRYAFDFARDKDQRSLDIDTAKSMLALLLGRTWPLFSVFYQYLE
QSKYRVMNKDQWYNVLEFSRTVHADLSNYDEDGAWPVLLDEFVEWQKVRQT

15

20

25

30

35

S (SEQ ID NO:422), PTRTDISSFKNIYRYAFDFARDKDQRSL (SEQ ID NO:423), SMLALLLGRTWPLFSVFYQYLE QSKYRVM (SEQ ID NO:424), FSRTVHADLSN YDEDGAWPVLLDEFVE (SEQ ID NO:425), IYRYAFDFAR (SEQ ID NO:426), KD QRSLDI (SEQ ID NO:427), NVLEFSRT (SEQ ID NO:428), and/or DLSNYDEDGA WPVLLDEFVEW (SEQ ID NO:429). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 11. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 11.

This gene is expressed primarily in aortic endothelium, and to a lesser extent, in cancers.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, endothelial disorders, particularly abnormalities of the vascular system and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., endothelial, vascular, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:157 as residues: Arg-22 to Lys-31.

The tissue distribution in aortic endothelium indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment, detection, and/or prevention of abnormalities of the vascular system (i.e. embolism, atherosclerosis, aneurysm, stroke, microvascular disease, etc.) and cancers. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:43 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

10

15

20

25

30

35

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 644 of SEQ ID NO:43, b is an integer of 15 to 658, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

Polypeptides of the invention do not comprise the polypeptide sequence shown as Genbank Accession W59652, which is hereby incorporated herein by reference. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: LFRCPIGKAGTPAGXGPEFPGRPTRPVREKELTETFE (SEQ ID NO:430), FFVFPYPYPFRPLPPIPFPRFPWFRRNFPIPIPESAPTTPLPSEK (SEQ ID NO:432), PWFRRNFPIPIPESAPTTPLP (SEQ ID NO:433), and/or GKAGTPAGXG PEFPGRPTRPV (SEQ ID NO:431). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in Hodgkin's lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, particularly Hodgkin's lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:158 as residues: Ser-21 to Asp-35, Pro-47 to Pro-52, Pro-62 to Asn-67.

The tissue distribution in Hodgkin's lymphoma tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of Hodgkin's lymphoma. Moreover, polynucleotides and

polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic-related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex- vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:44 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 552 of SEQ ID NO:44, b is an integer of 15 to 566, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 35

When tested against U937 and K562 cell lines, supernatants removed from cells containing this gene activated both the GAS (gamma activating sequence), and the ISRE (interferon-sensitive responsive element) promoter elements. Thus, it is likely that this gene activates pro-myeloid, leukemic, or more generally, other cells or cell-types, through the JAK-STAT signal transduction pathway. GAS is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells. ISRE is a promoter element found upstream in many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a

15

20

30

15

20

25

30

35

large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. The translation product of this gene was shown to have homology to a conserved trypsin inhibitor which is thought to play an essential role in protein metabolism and regulation (See Genbank Accession No. pirlS35098|S35098). In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

FYPPMTQGKESLPLLALQIFNTTFRPSFAFFSGHRTLFFGVRSPNPPKPRIFLIW LIAVAL (SEQ ID NO:434), LLALQIFNTTFRPSFAFFSGHRTLFFGVRSP (SEQ ID NO:435), HLAQTVMMHPQKSFYQVKNTNHSDRGAIEETQILEDRLGQIPLCLES QIWEA (SEQ ID NO:436), KNTNHSDRGAIEET QILEDRLGQIPLCL (SEQ ID NO:437), QGCYRRDS NIGRQVRPDSIMLRKPDLGSITHYGSVLGNLNYCDLP QLYRNPSLGNSGMREMFSPFYNPVECHP (SEQ ID NO:438), PDSIMLRKPD LGSITHYGSVLGN (SEQ ID NO:439), and/or YRNPSLGNSGMREMFSPFYNPV (SEQ ID NO:440). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in brain frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural disorders, particularly disorders of the central nervous system or endocrine system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system or endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in brain frontal cortex, combined with the detected GAS and ISRE biological activities indicates polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of disoders of the central nervous system, caused by trauma, inflammation, demyelination, neoplasia, and degenerative diseases. Additionally, the molecule may function as a neuropeptide or hormone.

Moreover, considering the homology to a trypsin inhibitor and its localization in the brain, indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, 5 encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and 10 perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above 15 listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:45 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1263 of SEQ ID NO:45, b is an integer of 15 to 1277, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

30

35

25

20

The translation product of this gene was found to have homology to a zinc finger protein from Mus musculus (See Genbank Accession No. gnllPIDle225687) which is thought to be involved in the modulation of gene regulation. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: NSARGLSGGHPFPWLSEGHPF (SEQ ID NO:441), TDSDLTLGILLLGI YTNHIWEMFLAASRINSPKLEPEKSVKRQINFPSSKDVGCSLEVPKDGPPL SHGKEWIPLSHRKGWIPLSHMKGWPSLSHGKGWPP LSPRAEF (SEQ ID

10

15

20

25

30

35

NO:442), LGILLLGIYTNHIWEMFLAA (SEQ ID NO:443). KSVKRQINFPSSKDV GCSLEVPKDGPP (SEQ ID NO:444), GKEWIPLSHRKGWIPLSHMKGWPSLSH (SEQ ID NO:445), GWASTQPRERMDPAQPQERMDPSQPHERMALTQPWKRMAP TQPSCRI (SEQ ID NO:446), and/or PAQPQERMDPSQPHERMALTQPWK (SEQ ID NO:447). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders. Similarly, polypeptides and antibodics directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred cpitopes include those comprising a sequence shown in SEQ ID NO:160 as residues: Ser-30 to Asp-39.

The tissue distribution in neutrophils indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of immune disorders involving neutrophils, including neutropenia. The expression of this gene product indicates a role in regulating the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases. or autoimmunity disorders. such as autoimmune infertility, lense tissue

injury, demyelination, systemic lupus erythematosis, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. The protein product of this gene can be used in the preparation of therapeutic compositions, for treating, preventing or delaying the recurrence of a tumour or neuronal disorders, e.g. genetic diseases or acquired degenerative encephalopathies such as Alzheimer's disease. Moreover, the protein is also useful in the induction or inhibition of cellular apoptosis resulting in inhibition of tumour cell growth, to suppress tumour formation, to induce G1 arrest of the cell cycle and to act as nuclear transcription factor. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:46 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 428 of SEQ ID NO:46, b is an integer of 15 to 442, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:46, and where b is greater than or equal to a + 14.

25

30

35

10

15

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

When tested against U937 and K562 cell lines, supernatants removed from cells containing this gene activated both the GAS (gamma activating sequence), and the ISRE (interferon-sensitive responsive element) promoter elements. Thus, it is likely that this gene activates pro-myeloid, leukemic, or more generally, other cells or cell-types, through the JAK-STAT signal transduction pathway. GAS is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells. ISRE is a promoter element found upstream in

10

15

20

25

30

35

many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. The protein product of this gene was found to have homology to the G-protein coupled receptor TM1 long consensus polypeptide (See Genbank Accession No. R50790) which indicates the protein is useful in the modulation of signalling events, cell-cycle regulation and/or transcriptional regulation. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: IANGGGRPIKLNALYK IQNECKIVFTCIDF (SEQ ID NO:448), and/or MPCIK SKMNAKLFSLVLTLCCMIPISVLFGTCI (SEQ ID NO:449). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in duodenum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, gastrointestinal diorders, particularly abnormalities of the duodenum. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., gastrointestinal, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in duodenum, the homology to the TM1 g-protein coupled receptor consensus sequence, in addition to the detected GAS and ISRE biological activities, indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of the abnormalities of the duodenum, particularly proliferative conditions such as cancers. Moreover, the protein can be used in G-protein coupled receptor ligand binding assays. The assay can be used to identify fragments from GPR proteins (see Genseq Accession Nos. R48686-R48758 for examples) which retain biological activity such as binding a GPR ligand or

WO 99/31117

5

10

15

modulating GPR ligand binding to a GPR (see Genseq Accession Nos. R48759-R48758, R50569-R50807 and R89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:47 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 876 of SEQ ID NO:47, b is an integer of 15 to 890, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a + 14.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 38

The translation product of this gene shares sequence homology with a growth and transformation dependent protein (>gil207250), which is thought to be important in the regulation of cellular growth and proliferation. In specific embodiments,

- polypcptides of the invention comprise the following amino acid sequence: QVAMGSLSGLRLAAGSCFRLCERDVSSSLRLTRSSDLKRINGFCTKPQESPG APSRTYNRVPLHKPTDWQKKILIWSGRFKKEDEIPETVSLEMLDAAKNK (SEQ ID NO:450), GLRLAAGSCFRLCERDVSSSLRLTR (SEQ ID NO:451), APSRTYNR VPLHKPTDWQKK (SEQ ID NO:452), IWSGRFKKEDEIPETVSLEMLDA (SEQ ID
- 30 NO:453), MDFAQNHRKVPELHPALTTECLYTNLRIGRKRSSYGQVASKRKM KSQRLSRWRCLMLQRTRCE (SEQ ID NO:454), KVPELHPALTTECLYTNLR (SEQ ID NO:455), KRSSYGQVASKRKMKSQRLSRWRCLM (SEQ ID NO:456), INGFCTKPQESP (SEQ ID NO:457), RVPLHKPTD (SEQ ID NO:458), WSGRFK KE (SEQ ID NO:459), EMLDAAKNK (SEQ ID NO:460), SYLMIALTV (SEQ ID
- NO:461), and/or MVIEGKKAA (SEQ ID NO:462). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive, or endocrine disorders, particularly abnormalities of the ovary. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, endocrine, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:162 as residues: Lys-25 to Thr-33, Leu-39 to Glu-47.

The tissue distribution in ovary, combined with the homology to the growth and transformation dependent protein, indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of the abnormalities of the ovary such as ovarian cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:48 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 723 of SEQ ID NO:48, b is an integer of 15 to 737, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a + 14.

10

15

20

25

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: RPGMRALGSCLSLLALCSPQARPGPRTLDASTATLTPHF SPCARFSPVGPSAVPFAATPLPLAGPHQP (SEQ ID NO:463), GSCLSLLALCS PQARPGPRT (SEQ ID NO:464), HFSPCARFSPVGPSAVPFAATPL (SEQ ID NO:465), AIEERNKSRLTQQASEPTGSPRYLHEQHPGSRSQMDCGSLTMXCPPP RVRDDRTSARGVPRQAAPDIVGGRPSSRACVSXPACAPSAAVFPY (SEQ ID NO:466), LTQQASEPTGSPRYLHEQHPGSRS (SEQ ID NO:467), and/or SARG VPRQAAPDIVGGRPSSRACVS (SEQ ID NO:468). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in ovarian tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive or endocrine disorders, particularly ovarian tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the female reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, endocrine cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:163 as residues: Met-1 to Gly-6, Trp-23 to Arg-29, Ala-38 to Ser-45.

The tissue distribution in ovarian tumor tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of reproductive disorders, particularly ovarian conditions, such as tumors. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:49 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the

scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 557 of SEQ ID NO:49, b is an integer of 15 to 571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:49, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 40

10

15

20

25

30

35

5

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: PRVRKTPHLSASGK (SEQ ID NO:469), YYYSMLKICHITI LETLSDRTPRKFAK KCYILYIKLSDSSVEKVAYTLLLLIPAAIEKK (SEQ ID NO:470), and/or TILETLSDRTPRKFAK KCYILYIKLSDSSVEK (SEQ ID NO:471). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in endometrial stromal cells treated with estradiol.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive disorders, particularly cancer of the endometrium. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, endometrial, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:164 as residues: Met-1 to Ser-7.

The tissue distribution in endometrial stromal cells indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of diseases of the endometrium, particularly cancer or diseases caused by hormonal imbalances. Protein, as well as, antibodies directed against the protein may

10

show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:50 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 342 of SEQ ID NO:50, b is an integer of 15 to 356, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 41 15

The translation product of this gene shares sequence homology with the smaller hepatocellular oncoprotein which is thought to be important in protein synthesis leading to cellular transformation. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: VHTKEIFRERSAGFPVK (SEQ ID 20 NO:472), LEMGFQPTKEINARGSEPCQAQSTSLPKLPRWGSRPEAPQTPQGG LESRCCTPVSKQSLNLKADRFKALTLGRAQWLT PVIQALSELRWVDHLRSGV (SEQ ID NO:473), FQPT KEINARGSEPCQAQSTSLPK (SEQ ID NO:474), PKLPR WGSRPEAPQTPQGGLESRCCTP (SEQ ID NO:475), and/or RFKALTLGRAQWLT PVIQALSELRWVD (SEQ ID NO:476). Polynucleotides encoding these polypeptides 25 are also encompassed by the invention.

This gene is expressed primarily in human bladder.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are 30 not limited to, urogenital disorders, particularly proliferative conditions, such as bladder tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bladder, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., urogenital, bladder, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal

10

15

20

fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:165 as residues: Pro-30 to Lys-38, Pro-45 to Ile-60, Leu-79 to Ser-96, His-98 to Gly-118.

The tissue distribution in bladder tumors indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of carcinomas and preneoplastic or pathological conditions of bladder, or of the urogenital/renal system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:51 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 899 of SEQ ID NO:51, b is an integer of 15 to 913, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

25

30

35

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: RIPLQSDGSFLHEKSSQQRSNRNFPCPTLQCNPEVSFWFV VTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTLAPPMDPS VPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIP SDPLDMKG GHINDAFMTEDERLTPL (SEQ ID NO:477), PCPTLQCNPEVSF WFVVTDPSKNHT (SEQ ID NO:478), AIRMNKNRINNAFFLNDQTLEFL (SEQ ID NO:479), IWQRRRKNKEPSEVDDAEDKCENM (SEQ ID NO:480), PLDMKG GHINDAFMTEDER (SEQ ID NO:481), GSRTTALQRGVSLSSSVMKASLICPP FMSRGSEGMPFSIVIMFSHLSSASSTSDGSLFFLLRCQIPDKISSAIATMM MQNITPNIIIQMGTDGSMGGASVEGIFKNSRVWSFRKKALLIRFLFILMADCTST A GRV (SEQ ID NO:482), VSLSSSVMKASLICPPFMSRGSEGMPFS (SEQ ID

10

15

20

25

30

35

NO:483), and/or SMGGASVEGIFKNSRVWSFRKKAL (SEQ ID NO:484). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in kidney, and to a lesser extent, in gall bladder and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases of the renal, urogenital, or reproductive system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., renal, urogenital, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, seminal fluid, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder:

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:166 as residues: Lys-60 to Ala-66, Thr-78 to Ser-83.

The tissue distribution in kidney indicates the protein product of this gene could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilm's Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Moreover, the tissue distribution in gall bladder indicates that the protein is useful for the treatment, detection, and/or prevention of various metabolic disorders. Alternatively, the expression within testes indicates that the protein is useful in normal testicular function. Therefore, this gene product may be useful in the treatment of male infertility, and/or could be used as a male contraceptive. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:52 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

WO 99/31117

5

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1342 of SEQ ID NO:52, b is an integer of 15 to 1356, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 43

- In specific embodiments, polypeptides of the invention comprise the following 10 amino acid sequence: GARGSQQDAPALQEAEVRGPERAQPARGR (SEQ ID NO:485), SERPGEGPARPGQDDQGPAVPAVAGAGVGVHDPADHRVLGQRSAA HFYLHTSFSRPHTGPPLPTPGPDRTGSSRPTPMSTSFWTISHAGVKQSDLPRKE TEQPPAPGEHGGERERLRLVPARRPAQPRPGPAAGGAEERAAGLLRQLQP GLPHQGARIRRHPQLGAEPPDRGRPARGHLLLRAQGGLHQLEARDDRAER 15 KPAAPRCALPRPAAHPARARAQRQRAPDLQQVLAPLREALPPPHEGQAQEVHQ VPLRARPLRAPDLRLPQQVRAGERGVLPQVRRAHAAGVRQPHQPARLGAR GLPRWPQGVLRQLHPVPAGPAHGEAGALQRALAAGVPPLPPVPDRLRFLG KLETLDEDAAQLLQLLQVDRQSASPRATGTGPPAAGRRTGSPRSPWPGG SSCINSTRPTLFSSATPSPKTSSETESFRVAFSRVPGT (SEQ ID NO:486), RPGQ 20 DDQGPAVPAVAGAGVGVHDPA (SEQ ID NO:487), SRPHTGPPLPTPGPDRT GSSR (SEQ ID NO:488), SHAGVKQSDLPRKETEQPPAPGE (SEQ ID NO:489), RRPAQPRPGPAAGGAEERAAGLL (SEQ ID NO:490), RRHPQLGAEPPDRGR PARGHLLL (SEQ ID NO:491), RDDRAERKPAAPRCALPRPAAHPAR (SEQ ID NO:492), RAPDLQQVLAPLREALPPPHEGQAQEV (SEQ ID NO:493), DLRLPQQ 25 VRAGERGVLPQVRRAHAAG (SEQ ID NO:494), QPARLGARGLPRWPQGVLR QLHPVPAG (SEQ ID NO:495), AGVPPLPPVPDRLRFLGKLETLDE (SEQ ID NO:496), QLLQLLQVDRQSASPRATGTGPPAA (SEQ ID NO:497), NSTRPTLFSS ATPSPKTSSETESFR (SEQ ID NO:498), LGGKRTAGPPGVAAAAARRPRPE SPASPGIVVDLARVAEAVHLPPVLVEGRQLLRVRVQQVLDEVGEGHLEASA 30 EGLARRGGQAGVVGVHPQHGHGELAVELLVLQLELAAEGGDQAHEGVAHEE ELGVLLELDLHEVAGELPVAAPELVEGQVRAGVVHVLARDAQRVAVGRTA VQQASAQHDHHALPVGAGHLGHVAVDGPVPVVHDQVAQLRVGDVVECALLG
- GEGQAGVGAEAPQHVPPLRLLPALVWAAPGVARGPVVASHALLHAPPA

 35 QAAAPSPFWEGHSASRQHEKLSRNSSTSESAVSS LSCPARAWAAAAPCAA
 (SEQ ID NO:499), EAVHLPPVLVEGRQLLRVRVQQV (SEQ ID NO:500), GHLEA
 SAEGLARRGGQAGVVGVHP (SEQ ID NO:501), QLELAAEGGDQAHEGVAHE

EELGVLLEL (SEQ ID NO:502), GELPVAAPELVEGQVRAGVVHVLARDA (SEQ ID NO:503), AVQQASAQHDHHALPVGAGHLGHVA (SEQ ID NO:504), ALVW AAPGVARGPVVASHALLHA (SEQ ID NO:506), HDQVAQLRVGDVVECALLG GEGQAG (SEQ ID NO:505), PPAQAAAPSPFWEGHSASRQHEKLSRNS (SEQ ID NO:507), SRVTFPERRRSSRLRRGSMEESVRGYDWSPRDARRSPDQGRQQAERRNVLRGFCANSSLAFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKV ACTNWKRVMIVLSGSLLHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGK LSRHLMKVKLKKYTKFLFVRDPFVRLISAFRSKFELENEEFYRKFAVPMLRVY ANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKLAPFNEHWRQVYRLC HPCQIDYDSWGSWRLWTRTPRSCCSYSRWTGSPLPPELPEQDRQQLGGGLVR10 QD PPGLEAAAV (SEQ ID NO:508), RSPDQGRQQAERRNVLRGFCANSSLA (SEQ ID NO:509), TKERAFDDIPNSELSHLIVDDRHGAIYC (SEQ ID NO:510), FNKFWRRYGKLSRHLMKVKLKKY (SEQ ID NO:511), FVRLISAFRSKFELE NEEFYRKFA (SEQ ID NO:512), TSLPASAREAFRAGLKVSFANFIQYL (SEQ ID NO:513), and/or SYSRWTGSPLPPELPEQDRQQLGGG (SEQ ID NO:514). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 7. Accordingly, polynucleotides related to this invention are useful as a marker in linkage

It has been discovered that this gene is expressed primarily in PMA activated monocytic HL60 cells.

Therefore, nucleic acids of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of the following diseases and conditions: blood related disease such as leukemia. Similarly, polypeptides and antibodies directed to those polypeptides are useful to provide immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be detected in certain tissues (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID 35 NO:167 as residues: Ala-29 to Thr-37, Pro-39 to Leu-63.

The tissue distribution in HL60 cells suggests the protein product of this clone is useful for the diagnosis, treatment, and/or prevention of blood related diseases such

15

20

25

30

analysis for chromosome 7.

WO 99/31117

as leukemia. Moreover, the protein product of this clone is useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture,

5 bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:53 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1533 of SEQ ID NO:53, b is an integer of 15 to 1547, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:53, and where b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 44

When tested against fibroblast cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) promoter element. Thus, it is likely that this gene activates fibroblasts, or more generally, other cells or cell types, through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jak-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation. The gene encoding the disclosed cDNA is believed to reside on chromosome 12. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 12. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: STGCSE (SEQ ID NO:515),

15

20

30

15

CLCLGCGLPELHSYLDPGPYLLVYPTLFWLCPSAVSPWAYTCYQLGLGPQWGA
AALSFTVDAAIRVWDVSTETCVPLPWFRGGGVTNCSGPQTAAKSWLPLLQLSF
ESGRPRCGLVRGGLLYQGAVRLAA GAQMAADCCSLYWESH (SEQ ID
NO:516), YPTLFWLCPSAVSPWAYTCYQLGLGP (SEQ ID NO:517), DVSTETCVP
LPWFRGGGVTNCSGPQ (SEQ ID NO:518), LLYQGAVRLAA GAQMAADCCSL
(SEQ ID NO:519), NKRKTYLFLEVGMWGVGQNRWWPWERVPRGRGWGCL
SKEGQVMNRASTPSRGFLGPPKHWAKTWKLGIDKVQRDVGNSACGPAH
TEQGPFVEGRWKVMSWGWAPGSPWIMPQGRSSNTGLFRVRKRRMTGLPS
CTLGFPFISTARRSPLGSQTME (SEQ ID NO:520), GVGQNRWWPWERVPRG
RGWGCLSKEG (SEQ ID NO:521), AKTWKLGIDKVQRDVGNSACGPAHTE
(SEQ ID NO:522), and/or WAPGSPWIMPQGRSSNTGLFRVRKRRMTGLPSC
TLGFPFIST (SEQ ID NO:523). Polynucleotides encoding these polypeptides are also
encompassed by the invention.

This gene is expressed primarily in fetal tissues such as fetal brain, fetal liver, fetal kidney, and to a lesser extent, in T cells and macrophages.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, blood-related, immuno-related, neural-related, or developmental 20 disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoesis and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, 25 immune, hematopoietic, urogenital, renal, hepatic, metabolic, developmental, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, amniotic fluid, bile, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the 30 disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:168 as residues: Cys-126 to Thr-138, Glu-165 to Gly-172, Thr-189 to Leu-200, Gly-222 to Gly-229, Pro-346 to Lys-354.

The tissue distribution in fetal liver indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of blood related diseases, particularly immune or hematopoietic disorders. Alternatively, the expression within fetal brain indicates polynucleotides and polypeptides

10

15

20

25

30

35

corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Alternatively, the expression within fetal kidney indicates the protein product of this gene could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilm's Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Moreover, the expression within various fetal tissues, combined with the detected EGR1 biological activity, indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:54 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1324 of SEQ ID NO:54, b is an integer of 15 to 1338, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:54, and where b is greater than or equal to a + 14.

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: SSYQCPKVTFFKSSVDT (SEQ ID NO:524). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 15. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 15.

This gene is expressed primarily in glioblastoma, liver, fetal lung, and amygdala.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural, metabolic, or developmental disorders, particularly mental or neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, metabolic, developmental, pulmonary, hepatic, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, amniotic fluid, pulmonart surfactant or sputum, bile, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:169 as residues: Pro-31 to Ala-37, Lys-62 to Asn-72.

The tissue distribution in glioblastoma and amygdala indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of central nervous system disorders. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder,

10

15

20

learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. The protein may also be useful in the treatment, detection, and/or prevention of liver disorders, which include, but are not limited to hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells. In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various would-healing models and/or tissue trauma. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:55 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2057 of SEQ ID NO:55, b is an integer of 15 to 2071, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where b is greater than or equal to a + 14.

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 46

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: YIYSYLGFFNQINK (SEQ ID NO:525). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed in only T-cell helper II cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, particularly infectious diseases, inflammatory, or immunodefiency conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

10

15

20

25

30

35

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:170 as residues: Pro-44 to Tyr-49.

The tissue distribution in T-helper cells indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment of infectious diseases. Moreover, the expression of this gene product indicates a role in regulating the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosis, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:56 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1885 of SEQ ID NO:56, b is an integer of 15 to 1899, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where b is greater than or equal to a + 14.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 47

The translation product of this gene has been shown to have homology to the
human nuclear factor IV (See Genbank Accession No. gil35038), which is thought to
play a role as a type 2 DNA helicase in DNA metabolism either during transcription,
DNA repair, and/or during the cell-cycle. Moreover, the protein may play a role in
chromosomal translocations. In specific embodiments, polypeptides of the invention
comprise the following amino acid sequence: ARDLIL (SEQ ID NO:526), LTFYL

QFLAPKDKPSGDTAAVFEEGGDVDDLVSTFNMHLVFCD (SEQ ID NO:527),
and/or FLAPKDKPSGDTAAVFEEGGDVDDL (SEQ ID NO:528). Polynucleotides
encoding these polypeptides are also encompassed by the invention. The gene encoding
the disclosed cDNA is believed to reside on chromosome 2. Accordingly,
polynucleotides related to this invention are useful as a marker in linkage analysis for
chromosome 2.

This gene is expressed primarily in activate T-cells, and to a lesser extent, in B-cells and monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or hematopoietic disorders, particularly leukemia, Grave's disease, rheumatoid arthritis and other autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25

30

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:171 as residues: Gly-27 to Cys-35.

The tissue distribution in T-cells, B-cells, and monocytes indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment or diagnosis of immune system diseases. Moreover, the expression of this gene product indicates a role in regulating the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versushost diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosis, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:57 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1529 of SEQ ID NO:57, b is an integer of 15 to 1543, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where b is greater than or equal to a + 14.

35

30

5

10

15

20

analysis for chromosome 14.

5

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: ARAGAKILFEGEF (SEQ ID NO:529), NFEIHSAFPFMLFVA CLLHSSCPRTARFLASPLSESNVIFYQNQYQFPCILCFIEFARLTSFKHLIHSQSH LVRLQYEDFSVSSE AWDTELT (SEQ ID NO:530), FPFMLFVACLLHSSCPRTA RFLASPL (SEQ ID NO:531), NVIFYQNQYQFPCILCFIEFARLTSF (SEQ ID NO:532), and/or SQSHLVRLQYEDFSVSSE AWDTE (SEQ ID NO:533). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 14. Accordingly, polynucleotides related to this invention are useful as a marker in linkage

This gene is expressed primarily in fetal tissues such as fetal liver, fetal brain, fetal lung and fetal spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental disorders and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., developmental, hepatic, immune, hemaopoietic, neural, pulmonary, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, amniotic fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:172 as residues: Gly-37 to Asp-46, Ser-48 to Val-54.

The tissue distribution in fetal tissues indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of developmental disorders and cancers. Moreover, the expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. The protein is also useful in the treatment, detection, and/or prevention of immune, hematopoietic,

pulmonary, or metabolic diseases, disorders, and/or conditions. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:58 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1119 of SEQ ID NO:58, b is an integer of 15 to 1133, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 49

20

15

5

10

The translation product of this gene was found to have homology to a 35kd pulmonary surfactant protein, as well as, a GABA-like receptor (See Genbank Accession Nos. P70663, and gil540271, respectively), the latter of which is thought to be important in neuronal function. In specific embodiments, polypeptides of the 25 invention comprise the following amino acid sequence: QKFLCASDGD (SEQ ID NO:534), AEVPLRVRRRHGRPHGPGGRQLALGIPALRSLPGCVPRHHGC SPGYGCLHRRILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGF EASPPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFF PSLDPVPDSPNFEVIXPXWGTVGCCGWVWGRCI (SEQ ID NO:535), GPGG 30 RQLALGIPALRSLPGCVPRHHGC (SEQ ID NO:536), FEASPPAQGIPEAK VRHPLSYVAQR (SEQ ID NO:537), DMSLGMWQHQWDKMDTGPPSQAPD TGHGGETSPPWHALGSPVLPEAALLSDFLFVPQWLWGQACLPTGHRHLPQLPP TSSF SEDLSTG (SEQ ID NO:538), PPSQAPDTGHGGETSPPWHALGS (SEQ ID NO:544), PVDRSSEKLLVGGSWGRWRWPVGRQAWPQSHCGTKRKSDRR 35 AASGKTGEPSACHGGEVSPPCPVSGAWEG GPVSILSH (SEQ ID NO:539). PVDRSSEKLLVGGSWGRWRWPV (SEQ ID NO:540), TKRKSDRRAASG KTGEPSACHGGEV (SEQ ID NO:541). MTSKFGESGTGSRDGKKTSPGPG

10

15

20

25

30

35

GDRGVLGSESRCRPDSEGCRWAT (SEQ ID NO:542), and/or SPGPGGDRGV LGSESRCRPD (SEQ ID NO:543). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in hematopoiesis cells such as neutrophils, eosinophils and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, blood diseases and/or immune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoeitic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:173 as residues: Ser-44 to Ala-63, Pro-89 to Gly-98, Pro-129 to Trp-137.

The tissue distribution in neutrophils, eosinophils, and T cells indicates polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosis blood related diseases. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. The homology to a pulmonary surfactant protein indicates that the protein is useful in enhancing or inhibiting the efficacy of the immune response across mucosal barriers, such as within the gastrointestinal tract, the sinuses, and the lungs. Protein, as well as, antibodies directed against the protein may

10

show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:59 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1476 of SEQ ID NO:59, b is an integer of 15 to 1490, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 50

When tested against U937 cell lines, supernatants removed from cells containing this gene activated the GAS (gamma activating sequence) promoter element. Thus, it is likely that this gene activates promyeloid cells, or more generally, other cells of the immune or central neurvous system, through the JAK-STAT signal transduction 20 pathway. GAS is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS 25 element, can be used to indicate proteins involved in the proliferation and differentiation of cells. The gene encoding the disclosed cDNA is believed to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: HEVQPSYLPSNSGLI (SEQ ID NO:545). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in the central nervous system, adult liver, adult heart, and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural, cardiovascular, or metabolic conditions or disorders. Similarly,

30

10

15

20

25

30

35

polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, cardiovascular, developmental, metabolic, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, amniotic fluid, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tissues of the CNS and infant brain, combined with the detected GAS biological activity indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of CNS disorders. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. The expression within fetal tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:60 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the

scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1322 of SEQ ID NO:60, b is an integer of 15 to 1336, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 51

10

15

20

25

30

35

5

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: LRISVLCRETACNWSHHPLDSN (SEQ ID NO:546). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 18. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 18.

This gene is expressed in whole brain, embryos, fetal liver and fetal spleen, and melanocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural, immune, hematopoietic, or developmental disorders, particularly mental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, immune, hematopoietic, developmental, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, amniotic fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:175 as residues: Pro-27 to Lys-42.

The tissue distribution in brain indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of mental or neurodegenerative disorders. Alternatively, the expression within fetal

15

20

25

liver/spleen indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. The protein may also be useful for the treatment and/or detection of metabolic disorders, which include Tay-Sachs disease, phenylkenonuria, galactosemia, hyperlipidemias, porphyrias, and Hurler's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:61 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1691 of SEQ ID NO:61, b is an integer of 15 to 1705, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:61, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

When tested against U937 and fibroblast cell lines, supernatants removed from cells containing this gene activated both the GAS (gamma activating sequence) and EGR1 (early growth response gene 1) promoter elements. Thus, it is likely that this gene activates promyeloid cells, fibroblasts, or more generally, immune or integumentary cells or cell-types, through the JAK-STAT and/or EGR1 signal transduction pathway. GAS is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells.

10

15

20

25

30

35

Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells. EGR1 is a separate signal transduction pathway from Jak-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: LTVTVRNPGSTHASGRPRRRSGVWARRGLVWQ (SEQ ID NO:547). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in endometrial stromal cells and fetal brain tissue, and to a lesser extent, in microvascular endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive, neural, developmental, or vascular disorders, particularly vascular leak syndrome and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endothelium, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, neural, developmental, vascular, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, amniotic fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:176 as residues: Pro-63 to Cys-72, Gly-88 to Cys-93.

The tissue distribution in endometrial stromal cells, infant brain, and microvascular endothelial cells, combined with the detected GAS and EGR1 biological activities, indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment of various vascular disorders, which include, but are not limited to vascular leak syndrome, microvascular disease, atherosclerosis, aneurysm, stroke, embolism and inflammation. Moreover, the expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could

again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:62 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1017 of SEQ ID NO:62, b is an integer of 15 to 1031, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where b is greater than or equal to a + 14.

15

20

25

30

35

10

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

Contact of cells with supernatant expressing the product of this gene has been shown to increase the permeability of the plasma membrane of HUVEC cells to calcium. Thus, it is likely that the product of this gene is involved in a signal transduction pathway that is initiated when the product binds a receptor on the surface of the plasma membrane of both vascular endothelial cells, in addition to other cell-lines or tissue cell types. Thus, polynucleotides and polypeptides have uses which include, but are not limited to, activating endothelial cells, or more generally, neural or immune cells. Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium and sodium, as well as alter pH and membrane potential. Alterations in small molecule concentration can be measured to identify supernatants which bind to receptors of a particular cell. This protein is homologous to members of the butyrophilin gene family which are thought to play a role in myelin sheath development, in addition to serving as a membrane-specific receptor for cytoplasmic vesicles to the apical plasma membrane. In specific embodiments, polypeptides of the invention comprise the sequence SAQFSVLGPSGPILAMVGEDADLPCHLFPTMSAETMELKW (SEQ ID NO:574). Polynucleotides encoding these polypeptides are also encompassed by the invention. In specific embodiments, polypeptides of the invention comprise the sequence TPCSAQFSVLGPSGPILAMVGEDADLPCHLFPTMSAET (SEQ ID NO:548), MELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRTSILRDGITAGKAALRIHN

VTASDSG (SEQ ID NO:549), LEVKGYEDGGIHLECRSTGWYPQPQI (SEQ ID NO:550), MASSLAFLLLNFHVSLLLVQLLTPCSAQFSVLGPSGPILAMVGE DADLPCHLFPTMSAETMELKWVSSSLRQVVNVYADG (SEQ ID NO:551), RHELSHNRKNGELLIDRLYSVGSDSPMGIPRDIIFTDGFPYWNPKVKTLKDRHF WQSIDENGKFPGFPSA QLSCLPPLGPAAHSLLSSVFCAWTLWAHPGHGG (SEQ ID NO:552), LLIDRLYSVGSDSPMGIPRDIIFT (SEQ ID NO:553), NPKVKT LKDRHFWQSIDENGKFPGF (SEQ ID NO:554), LGPAAHSLLSSVFCAWTLWA HPGH (SEQ ID NO:555). RLQHWVLIFTLEVKGYEDGGIHLECRSTGWYPQP QIQWSNAKGENIPAVEAPVVADGVGLYEVAASVIMRGGSGEGVSCIIRNSLL GLEKTASISIADPSSGAPSPGSQPWQGPCLSCCCFSPEPVTSCGDNRRK (SEQ 10 ID NO:556), GGIHLECRSTGWYPQPQIQWSNAKG (SEQ ID NO:557), PQIQWS NAKGENIPAVEAPVVADGVGL (SEQ ID NO:558), NIPAVEAPVVADGVGL YEVAASVIMRG (SEQ ID NO:559), SGAPSPGSQPWQGPCLSCCCFSPEPVT (SEQ ID NO:560), SSSICDHERRLRGGCILHHQKFPPRPGKDSQHFHRRP FFRSAQPWIAALAGTLPILLLLAGASYFLWRQQKEITALSSEIESEQEMKE 15 MGYAATEREISLRESLQEELKRKKIQYLTRGEESSSDTNKSA (SEQ ID NO:561), KDSQHFHRRPFFRSAQPWIAALAGTLPI (SEQ ID NO:562), EIESEQEMKE MGYAATEREISLRESLQE (SEQ ID NO:563), VNNMIAFYSARDSYVYPHFSG EEMLQMRLHLVK (SEQ ID NO:564), TPCSAQFSVLGPSGPILAMVGEDADLP CHLFPTMSAET (SEQ ID NO:565), KWVSSSLRQVVNVYADGKEVEDR (SEQ ID 20 NO:566), RTSILRDGITAGKAALRIHNVTASD (SEQ ID NO:567), CYFQDGDFY EKALVELKVAALGS (SEQ ID NO:568), GYEDGGIHLECRSTGWYPQPQIQ (SEQ ID NO:569), NIPAVEAPVVADGVGLYEVAASV (SEQ ID NO:570), QQKEITALSS EIESEQEMKEM (SEQ ID NO:571), LRESLQEELKRKKIQYLTRGEESS (SEQ ID NO:572), and/or GEEMLQMRLHLVK (SEQ ID NO:573). Polynucleotides encoding 25 these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 6. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 6.

This gene is expressed primarily in rhabdomyosarcoma, and to a lesser extent, in T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, muscle, immune, or neural disorders, particularly rhabdomyosarcoma, infectious diseases, or neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

30

of the above tissues or cells, particularly of the immune system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., muscle, immune, neural, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:177 as residues: Ala-78 to Arg-94.

10 The tissue distribution in rhabdomyosarcoma, the detected calcium flux biological activity, combined with the homology to the butyrophilin gene family indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis or treatment of muscle disorders, which include, but are not limited to, muscular dystrophy, cardiomyopathy, fibroids, myomas, and/or rhabdomyosarcomas. 15 Moreover, the homology to the butyrophilin protein indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating 20 diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated 25 expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. The protein may also show utility in the correction or amelioration of myelin sheath deficiencies in developing and mature neurons and neural-cell types. Protein, as 30 well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:63 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

WO 99/31117 PCT/US98/27059

94

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1575 of SEQ ID NO:63, b is an integer of 15 to 1589, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is greater than or equal to a + 14.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 54

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: PQGGLTLPSVWG (SEQ ID NO:575), GGPCHLWLLGPRRT 10 QLPGRRASLPFRSQGELTQAFLLGLWKHQMPALTQEQQVRAERRREAVRMEI PGLFFASLANWGLLYRTSQDFISPYLCAAPSTPHPPLGGP (SEQ ID NO:576), GPRRTQLPGRRASLPFRSQGELT (SEQ ID NO:577), QMPALTQEQQVRAER RREAVRMEI (SEQ ID NO:578), and/or ANWGLLYRTSQDFISPYLCAAPSTP (SEQ ID NO:579). Polynucleotides encoding these polypeptides are also encompassed by the 15 invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 5. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 5.

This gene is expressed primarily in brain, and to a lesser extent, in testes tumor.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural, endocrine, or reproductive disorders, particularly depression and infertility disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification 25 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, endocrine, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, seminal fluid, synovial fluid and spinal fluid) 30 or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:178 as residues: Thr-26 to Glu-33.

The tissue distribution in brain indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of depression and

10

15

20

other endocrine-related disorders. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. The protein product may also be useful in the treatment, detection, and/or prevention of a variety of reproductive disorders which include, but are not limited to, the treatment of male infertility, and/or could be used as a male contraceptive. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:64 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1074 of SEQ ID NO:64, b is an integer of 15 to 1088, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where b is greater than or equal to a + 14.

30

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 55

The translation product of this gene was found to have homology to the conserved R166.2 protein from Caenorhabditis elegans (See Genbank Accession No.gil949849), which is thought to play an important role in the regulation of cellular function and processes. In specific embodiments, polypeptides of the invention comprise the sequence: LSFKDKSTYIESSTKVYDDMAFRYLSWILFPLLG (SEQ ID

WO 99/31117

NO:580), CYAVYSLLYLEHKGWYSWVLSM (SEQ ID NO:590), LLTFGFITMTPQ LFINYKLKSVAHLPWRMLT (SEQ ID NO:581), TYKALNTFIDDLFAFVIKMP VMYRIGCLRD (SEQ ID NO:582), DVVFFIYLYQRWIYRVDPTRVNEFGMSGED (SEQ ID NO:583), VAGIFPRLSFKDKSTYIESSTKVYDDMAFRYLSWILFPLLG CYA (SEQ ID NO:584), PWVAGIFPRLSFKDKSTYIESSTKVYDD (SEQ ID NO:586), AGEDSCHPVLSVQPDVHDLGWQESSPAYPSRTSPRISSPRPKC MMIWHSGTCPGSSSR SWAAMPSTVFCTWSTRAGTPGCSACSTASC (SEQ ID NO:587), LSVQPDVHDLGWQESSPAYPSRTSPRISSP (SEQ ID NO:588), GSSSR SWAAMPSTVFCTWSTRAGTP (SEQ ID NO:589), and/or WAAMPSTVFCTWS TRAGTP (SEQ ID NO:585). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 19. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 19.

This gene is expressed primarily in colon, smooth muscle and fetal bone.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, gastrointestinal or vascular disorders, and abnormal muscular-skeletal development, including proliferative conditions such as cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and musclar-skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., gastrointestinal, muscle, skeletal, vascular, developmental, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, amniotic fluid, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:179 as residues: Ser-128 to Thr-133, Thr-158 to Thr-166, Leu-168 to Gly-175, Ala-179 to Asp-196.

The tissue distribution in colon and fetal bone indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of abnormal bone formation, and/or various proliferative conditions (e.g. tumors), particularly of the gastrointestinal system. Moreover, the expression within smooth muscle tissue indicates polynucleotides and polypeptides corresponding to this gene are

15

20

25

30

10

15

20

25

30

35

useful for the detection, treatment, and/or prevention of a variety of vascular disorders, which include, but are not limited to the following: embolism, atherosclerosis, microvacular disease, aneurysm, stroke, and vascular leak syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:65 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1242 of SEQ ID NO:65, b is an integer of 15 to 1256, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:65, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: LGEFLSSQCFLP (SEQ ID NO:591). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in brain frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural disorders, particularly neurological or neurodegenerative disorders and diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10

15

20

25

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:180 as residues: Ala-122 to Gly-128.

The tissue distribution in brain frontal cortex indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of some neurological diseases such as depression. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:66 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1588 of SEQ ID NO:66, b is an integer of 15 to 1602, where both a and b correspond to the positions of nucleotide residues shown

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

in SEQ ID NO:66, and where b is greater than or equal to a + 14.

When tested against U937 cell lines, supernatants removed from cells

containing this gene activated the GAS (gamma activating sequence) promoter element.

Thus, it is likely that this gene activates pro-myeloid cells, or more generally, immune or hematopoietic cells, through the JAK-STAT signal transduction pathway. GAS is a

10

15

20

30

35

promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

RSRRNRVAMGMWASLDALWE (SEQ ID NO:592), PRVRCQQRAEGGMGAG IGVGPSERTDIAVTPRGRSEGASVGVAPVHAEGAGGTGWPWGCGHRWTLCG RCR PRSVSSGPCCSFPGQCIFGRPS (SEQ ID NO:593), GGMGAGIGVGPSER TDIAVTPRGR (SEQ ID NO:594), GCGHRWTLCGRCR PRSVSSGPCCSFP (SEQ ID NO:595), and/or KKHGF NQQTLGFFTWKYNKNKNLV (SEQ ID NO:596). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in synovial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, skeletal afflictions, particularly rheumatoid arthritis or autoimmune conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., skeletal, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:181 as residues: Gln-27 to Val-39, Glu-50 to Arg-56.

The restricted tissue distribution in synovium, combined with the detected GAS biological activity, indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of rheumatoid arthritis since synovial fibroblasts are associated with the synovium and cartilage. Moreover, polynucleotides and polypeptides corresponding to this gene are useful in the detection and treatment of disorders and conditions afflicting the skeletal system, in particular osteoporosis, bone

10

15

20

cancer, as well as, disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (i.e. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). The protein may also be useful in the modulation of the immune response to regions of inflammation, or in inhibiting or ameliorating autoimmune responses. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:67 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 924 of SEQ ID NO:67, b is an integer of 15 to 938, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

25

30

35

When tested against U937 cell lines, supernatants removed from cells containing this gene activated the GAS (gamma activating sequence) promoter element. Thus, it is likely that this gene activates pro-myeloid cells, or more generally immune or hematopoietic cells, in addition to other cells or cell-types, through the JAK-STAT signal transduction pathway. GAS is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: PKLLPCSPAEGHTSLGPLLPF (SEQ ID NO:597), ASLELXPS KSQLSTEWGFTWIVGLGMSPSTALWTECTCTPFLVLLSHASGHFFWLSPLAS

15

20

25

30

35

LVIPPVTDRK (SEQ ID NO:598), WGFTWIVGLGMSPSTALWTECTCTPFLVL LSH (SEQ ID NO:599), VAVGVCREDVMGITDRSKMSPDVGIWAIYWSAAGY WPLIGFPGTPTQQEPALHRVGVYLDRGTGNVSFYSAVDGVHLHTFSCS SVSRLRPFFLVESISIFSHSTSD (SEQ ID NO:600), ITDRSKMSPDVGIWAIYW SAAGYWPLI (SEQ ID NO:601), and/or RGTGNVSFYSAVDGVHLHTFSCSSV SRLRP (SEQ ID NO:602). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 7. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 7.

This gene is expressed primarily in fetal tissues, and to a lesser extent, in liver cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental or liver diseases, such as hepatocellular carcinoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hepatic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., developmental, hepatic, metabolic, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, bile, breast milk, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:182 as residues: Pro-30 to Gln-37, Arg-39 to Ser-45, Arg-74 to Arg-85.

The tissue distribution in liver, combined with the detected GAS biological activity indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment or diagnosis of hepatic conditions such as hepatocellular carcinoma. Moreover, the expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer

10

20

25

30

35

therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:68 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1571 of SEQ ID NO:68, b is an integer of 15 to 1585, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 59

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: GTRGLQNHRTE (SEQ ID NO:603). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in prostate, and to a lesser extent, in tonsil and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive, immune, developmental, or pulmonary disorders and/or diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, immune, developmental, pulmonary, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, amniotic fluid, pulmonary surfactant or sputum, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:183 as residues: Lys-32 to Lys-38.

The tissue distribution in prostate indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of cancers, particularly of the prostate. The expression within tonsils indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. The expression also indicates a role in regulating the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. Moreover, the expression within fetal tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:69 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1662 of SEQ ID NO:69, b is an integer of 15 to 1676, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:69, and where b is greater than or equal to a + 14.

25

30

35

10

15

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: ELSGLG (SEQ ID NO:604). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in the brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, central nervous system disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

10

15

20

25

30

35

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:184 as residues: Tyr-15 to Lys-21, Pro-62 to Phe-68.

The tissue distribution in brain indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of CNS disorders (such as Parkinson's disease). Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:70 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1330 of SEQ ID NO:70, b is an integer of 15 to 1344, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where b is greater than or equal to a + 14.

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

The gene encoding the disclosed cDNA is believed to reside on chromosome 3. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 3.

This gene is expressed primarily in the brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, CNS diseases, such as Alzheimers and Parkinson's disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:185 as residues: Asp-44 to Cys-53, Asp-56 to Lys-66, Ser-78 to Lys-84.

The tissue distribution in brain tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of CNS diseases such as Alzheimers and Parkinson's disease. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition.

homeostasis, or neuronal differentiation or survival. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:71 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1460 of SEQ ID NO:71, b is an integer of 15 to 1474, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where b is greater than or equal to a + 14.

15

20

25

30

35

10

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 62

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: MDDIKI (SEQ ID NO:605), NFCVSKNTFNRVKRPIKWVKIF ANDISCKRLISRIHKEILPFNNKKQPDFKVKKSRK (SEQ ID NO:606), FNRVKR PIKWVKIFANDISCKRLISRIHKE (SEQ ID NO:607), ETQMANKYMKRCSTL (SEQ ID NO:608), VIRELQVKATRRCHYTPIKWSKSKTLISSNADEYVEPTRTLI HCWWKCKIVQPLCKTAW (SEQ ID NO:609), and/or ATRRCHYTPIKWSKSKT LISSN (SEQ ID NO:610). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in duodenum, and to a lesser extent, in brain frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, gastrointestinal, neural, or endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., gastrointestinal, neural, endocrine, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal

10

15

20

25

30

fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in colon indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of some gastrointestinal disorders, particularly cancers. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioral disorders, or inflammatory conditions which include, but are not limited to Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, depression, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:72 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1998 of SEQ ID NO:72, b is an integer of 15 to 2012, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:72, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

This gene is expressed primarily in bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

10

15

20

25

30

biological sample and for diagnosis of diseases and conditions which include, but are not limited to, leukemia, immune deficiency syndromes, and other immune related diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of diseases of bone marrow, such as leukemia, bone cancer and immune deficiency syndrome. Furthermore, the polypeptides or polynucleotides are also useful to enhance or protect proliferation, differentiation, and functional activation of hematopoietic progenitor cells (e.g., bone marrow cells), useful in treating cancer patients undergoing chemotherapy or patients undergoing bone marrow transplantation. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:73 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:73, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where b is greater than or equal to a + 14.

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

When tested against sensory neuron cell lines, supernatants removed from cells containing this gene activated the EGR1 assay. Thus, it is likely that this gene activates sensory neuronal cells through a signal transduction pathway. Early growth response 1 (EGR1) is a promoter associated with certain genes that induces various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

This gene is expressed primarily in the testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive system-related diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., testes, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in testes indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of reproductive system-related diseases. Furthermore, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions concerning proper testicular function (e.g. endocrine function, sperm maturation), as well as cancer. Therefore, this gene product is useful in the treatment of male infertility and/or impotence. This gene product is also useful in assays designed to identify binding agents, as such agents (antagonists) are useful as male contraceptive agents. Similarly, the protein is believed to be useful in the treatment and/or diagnosis of testicular cancer. The testes are also a site of active gene expression of transcripts that may be expressed, particularly at low levels, in other tissues of the body. Therefore, this gene product may be expressed in other specific tissues or organs where it may play related functional roles in other processes, such as hematopoiesis, inflammation, bone formation, and kidney function, to name a few possible target indications.

10

15

20

25

30

35

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:74 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1734 of SEQ ID NO:74, b is an integer of 15 to 1748, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in synovial fibroblasts.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, rheumatoid arthritis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The restricted tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of rheumatoid arthritis, since synovial fibroblasts are associated with the synovium and cartilage. In addition, the expression of this gene product in synovium indicates a role in the detection and treatment of disorders and conditions afflicting the skeletal system, in particular osteoporosis as well as disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and

10

15

20

25

30

35

specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:75 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1556 of SEQ ID NO:75, b is an integer of 15 to 1570, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This gene is expressed primarily in ovarian cancer, and to a lesser extent in fetal tissues such as fetal liver and fetal brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers, particularly of the ovary. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., ovary, fetal, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:190 as residues: Pro-28 to Gln-33.

The tissue distribution in ovarian cancer tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of cancers; e.g., ovarian cancer, as well as other tissues where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:76 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 510 of SEQ ID NO:76, b is an integer of 15 to 524, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene is expressed primarily in testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, male reproductive or hormonal related disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., testes, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:191 as residues: Pro-68 to Asp-73, Gln-92 to Glu-107, Gln-120 to Lys-126.

The tissue distribution in testes indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of male

5

10

15

25

30

35

10

15

20

reproductive or hormonal disorders. Furthermore, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions concerning proper testicular function (e.g. endocrine function, sperm maturation), as well as cancer. Therefore, this gene product is useful in the treatment of male infertility and/or impotence. This gene product is also useful in assays designed to identify binding agents, as such agents (antagonists) are useful as male contraceptive agents. Similarly, the protein is believed to be useful in the treatment and/or diagnosis of testicular cancer. The testes are also a site of active gene expression of transcripts that may be expressed, particularly at low levels, in other tissues of the body. Therefore, this gene product may be expressed in other specific tissues or organs where it may play related functional roles in other processes, such as hematopoiesis, inflammation, bone formation, and kidney function, to name a few possible target indications. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:77 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1292 of SEQ ID NO:77, b is an integer of 15 to 1306, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where b is greater than or equal to a + 14.

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

When tested against U937 Myeloid cell lines, supernatants removed from cells containing this gene activated the GAS assay. Thus, it is likely that this gene activates myeloid cells through the Jak-STAT signal transduction pathway. The gamma activating sequence (GAS) is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

WO 99/31117

5

10

15

20

25

30

35

This gene is expressed primarily in human tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., tonsils, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the gene or protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:78 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1465 of SEQ ID NO:78, b is an integer of 15 to 1479, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where b is greater than or equal to a + 14.

5

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

This gene is expressed primarily in human thymus and six week old human embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, endocrine diseases and leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., endocrine, immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in thymus and developing embryonic tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of leukemia or other immune diseases, especially those which are involved in fetal development. Furthermore, the tissue distribution in thymus and developing embryonic tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancrease (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-,hypoparathyroidism), hypothallamus, and testes. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEO

ID NO:79 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1780 of SEQ ID NO:79, b is an integer of 15 to 1794, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where b is greater than or equal to a + 14.

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 70.

This gene is expressed primarily in adult pulmonary tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases of the cardiopulmonary system including asthma, bronchitis, apnea, enlarged heart, arythmia, strokes and heart attacks. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiopulmonary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., pulmonary, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:194 as residues: Pro-27 to Leu-41.

The tissue distribution in pulmonary tissues indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment or diagnosis of diseases such as arythmia, apnea, asthma and possibly for the early detection and prevention of patients likely to have strokes or heart attacks. Furthermore, the tissue distribution in pulmonary tissues indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of disorders associated with developing lungs, particularly in premature infants where the lungs are the last tissues to develop. Additionally, the tissue distribution indicates polynucleotides

and polypeptides corresponding to this gene are useful for the diagnosis and intervention of lung tumors. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:80 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1266 of SEQ ID NO:80, b is an integer of 15 to 1280, where both a and b correspond to the positions of nucleotide residues shown

15

10

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 71

in SEQ ID NO:80, and where b is greater than or equal to a + 14.

When tested against K562 leukemia cell lines, supernatants removed from cells containing this gene activated the ISRE assay. Thus, it is likely that this gene activates 20 leukemia cells through the Jak-STAT signal transduction pathway. The interferonsensitive response element is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the ISRE 25 element, can be used to indicate proteins involved in the proliferation and differentiation of cells. Furthermore, contact of cells with supernatant expressing the product of this gene increases the permeability of THP-1 monocyte cells to calcium. Thus, it is likely that the product of this gene is involved in a signal transduction pathway that is initiated when the product of this gene binds a receptor on the surface of the monocyte cell. 30 Thus, polynucleotides and polypeptides have uses which include, but are not limited to, activating monocyte cells.

This gene is expressed primarily in adult human spleen and adult human testis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to

35

10

15

20

these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., spleen, testes, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:195 as residues: Pro-32 to Gly-39.

The tissue distribution in spleen, in addition to the biological activity data, indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders. Furthermore, this gene may play a role in the survival, proliferation, and/or differentiation of hematopoietic cells in general, and may be of use in the augmentation of the numbers of stem cells and committed progenitors. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:81 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 960 of SEQ ID NO:81, b is an integer of 15 to 974, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:81, and where b is greater than or equal to a + 14.

30

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 72

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

35 ELSGLVIITAWIILCHSSSKNPVGGRIQLAIAIVITLFPFISWVYIYINKEMRSSWP THCKTVI (SEQ ID NO:611), QCPQGTETEAGVSVPPRKEGGGPYVAGLTAPHVA GLTAPRRVLRAMAPALWRACNGL (SEQ ID NO:612), HSSSKNPVGGRIQLA

10

15

20

25

30

35

IAIVITLFPFISWVYIY (SEQ ID NO:613), and/or RKEGGGPYVAGLTAPHVA GLTAPRRVLRAMAP (SEQ ID NO:614). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in liver tissues, and to a lesser extent in t-cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hepatitis, sclerosis of the liver and cancer of the liver. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in liver indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and possible treatment of diseases of the liver. Since it is primarily found in the liver, and with the additional expression seen in T-cells, it most likely deals with the immune response in the liver, for example to diseases like hepatitis, sclerosis and hepatocellular carcinoma. More generally, the tissue distribution in liver indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:82 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1941 of SEQ ID NO:82, b is an integer of 15

15

20

25

30

35

to 1955, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 73

The gene encoding the disclosed cDNA is thought to reside on chromosome 10. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 10.

This gene is expressed primarily in myeloid progenitor cells, and to a lesser extent in leukemic cells and eosinophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, leukimia and other blood diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoesis and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in immune tissues indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of leukemia. Furthermore, the polypeptides or polynucleotides are also useful to enhance or protect proliferation, differentiation, and functional activation of hematopoietic progenitor cells (e.g., bone marrow cells), useful in treating cancer patients undergoing chemotherapy or patients undergoing bone marrow transplantation. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:83 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

15

20

25

30

35

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 624 of SEQ ID NO:83, b is an integer of 15 to 638, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:83, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

10 The translation product of this gene shares sequence homology with "neurogenic secreted signaling protein (brn)" (see gil1150971) from Drosophila melanogaster which is thought to be important in the normal development of brain tissue. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: PGRPTRPAXAGLSSGGAAQEAPQADPRPWLAR (SEQ ID NO:615). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in the placenta and early embryonic tissue. Northern data has demonstrated that this gene is expressed in brain, stomach and colorectal adenocarcinoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, several types of disorders of the brain including epilepsy, mood disorders, any of a variety of types of mental retardation, and addictive disorders including alcohlism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., brain, stomach, colon, placental, embryonic, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:198 as residues: Gln-37 to Ala-42, Thr-51 to Ala-57, Pro-71 to His-79, Glu-124 to Arg-137, Ser-151 to Val-159.

WO 99/31117

The tissue distribution and homology to Drosophila melanogaster putative neurogenic secreted signaling protein (brn) indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment of various brain disorders as well as pre-natal testing for neuropathological conditions, such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, 5 dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders. Furthermore, the 10 tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the placenta. Specific expression within the placenta indicates that this gene product may play a role in the proper establishment and maintenance of placental function. Alternately, this gene product may be produced by the placenta and then transported to the embryo, where it 15 may play a crucial role in the development and/or survival of the developing embryo or fetus. Expression of this gene product in a vascular-rich tissue such as the placenta also indicates that this gene product may be produced more generally in endothelial cells or within the circulation. In such instances, it may play more generalized roles in vascular function, such as in angiogenesis. It may also be produced in the vasculature and have effects on other cells within the circulation, such as hematopoietic cells. It may serve to promote the proliferation, survival, activation, and/or differentiation of hematopoietic cells, as well as other cells throughout the body. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:84 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 845 of SEQ ID NO:84, b is an integer of 15 to 859, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where b is greater than or equal to a + 14.

25

30

35

for the above listed tissues.

10

15

20

25

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

The translation product of this gene shares sequence homology with a fatspecific secreted protein.

This gene is expressed primarily in the epididymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, metabolic disorders and male infertility. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., epididymus, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:199 as residues: Tyr-21 to Asp-40, Ser-58 to Arg-64, Thr-71 to Ser-76, Ser-106 to Thr-112.

Homology to a fat-specific gene indicates that this gene may also play a role in the treatment and/or detection of metabolic disorders such as obesity, diabetes, anorexia nervosa and bulemia. In addition, its expression primarily in the epididymus indicates a role in the treatment/detection of male fertility disorders such as infertility, low sperm count, spermatorrhea and spermiation. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:85 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1115 of SEQ ID NO:85, b is an integer of 15

15

20

25

30

35

to 1129, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:85, and where b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 76

The translation product of this gene shares sequence homology with Slit, a secreted Drosophila protein which plays a role in the development of axon pathway development in the central nervous system. The Slit protein is necessary for the normal development of the midline of the CNS, particularly the midline glial cells, and for the concommitant formation of the commisural axon pathways. The process is dependent on the level of SLIT protein expression. It appears that the SLIT protein is excreted by the midline glial cells, where it is synthesised and is eventually associated with the surfaces of axons that traverse them. Contact of cells with supernatant expressing the product of this gene increases the permeability of THP-1 monocyte cells to calcium. Thus, it is likely that the product of this gene is involved in a signal transduction pathway that is initiated when the product of this gene binds a receptor on the surface of the monocyte cell. Thus, polynucleotides and polypeptides have uses which include, but are not limited to, activating monocyte cells. Furthermore, when tested against U937 Myeloid cell lines, supernatants removed from cells containing this gene activated the GAS assay. Thus, it is likely that this gene activates myeloid cells through the Jak-STAT signal transduction pathway. The gamma activating sequence (GAS) is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in infant brain, and to a lesser extent in adult cerebellum and frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell

10

15

20

30

35

types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:200 as residues: Glu-25 to Lys-33, Glu-115 to Lys-120.

The tissue distribution primarily in brain and homology to Slit, a gene involved in axon pathway development, indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment/detection of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, spinal cord injury, brain injuries, crushed (optic) nerve, amytrophic lateral sclerosis, diabetes caused nerve damage, strokes, epilepsy, multiple sclerosis, paraplegia retinal degeneration, Huntingtons Disease, facial nerve damage, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:86 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2660 of SEQ ID NO:86, b is an integer of 15 to 2674, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

The translation product of this gene shares sequence homology with human endothelial cell multimerin, which is a secreted protein that binds to the extracellular matrix and is thought to be involved in hemostasis. Multimerin is a factor V/Va-binding protein and may function as a carrier protein for platelet factor V (J. Biol Chem 1995 Aug 4;270(31):18246-51). Contact of cells with supernatant expressing the product of this gene increases the permeability of THP-1 Monocyte cells to calcium. Thus, it is

WO 99/31117 PCT/US98/27059 126

likely that the product of this gene is involved in a signal transduction pathway that is initiated when the product of this gene binds a receptor on the surface of the monocyte cell. Thus, polynucleotides and polypeptides have uses which include, but are not limited to, activating monocyte cells.

This gene is expressed primarily in a variety of hematopoetic cells including Tcells, dendritic cells and B-cells as well as cells and tissues of epithelial and endothelial origin including healing wounds and keratinocytes, as well as placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, acute internal injury, blood clotting disorders and other disorders of hemostasis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hemostasis, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., endothelial, immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:201 as residues: Ala-43 to Trp-57, Ser-81 to Gly-88, Tyr-125 to Asp-134, Pro-141 to Gly-154, Val-172 to Glu-178, Lys-296 to Gly-305, Leu-307 to Arg-314, Thr-335 to His-341.

The tissue distribution in endothelial tissues, and the homology to human endothelial cell multimerin, indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders involving the vasculature. Elevated expression of this gene product by endothelial cells indicates that it may play vital roles in the regulation of endothelial cell function; secretion; proliferation; or angiogenesis. Furthermore, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the placenta. Specific expression within the placenta indicates that this gene product may play a role in the proper establishment and maintenance of placental function. Alternately, this gene product may be produced by the placenta and then transported to the embryo, where it may play a crucial role in the development and/or survival of the developing embryo or fetus. Expression of this gene product in a vascular-rich tissue such as the placenta also indicates that this gene

5

10

15

20

25

30

35

product may be produced more generally in endothelial cells or within the circulation. In such instances, it may play more generalized roles in vascular function, such as in angiogenesis. It may also be produced in the vasculature and have effects on other cells within the circulation, such as hematopoietic cells, as supported by the biological activity data mentioned previously. It may serve to promote the proliferation, survival, activation, and/or differentiation of hematopoietic cells, as well as other cells throughout the body. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:87 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1622 of SEQ ID NO:87, b is an integer of 15 to 1636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where b is greater than or equal to a + 14.

20

30

35

5

10

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 78

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

25 HYXSTPGRVPVRQFAAASTSGGPWVPGGXLEAPFQVAPSLSHSTPVFPGLI (SEQ ID NO:616). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in osteoblasts.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, degenerative conditions of the bone including arthritis and osteoporosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., skeletal, cancerous and wounded

10

15

20

tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:202 as residues: Thr-45 to Cys-50, Met-55 to Pro-60.

The tissue distribution in osteoblasts indicates polynucleotides and polypeptides corresponding to this gene are useful for treating degenerative conditions of the bone mediated by alterations in the activity ratio of osteoblasts and osteoclasts. Furthermore, elevated levels of expression of this gene product in osteoblastoma indicates that it may play a role in the survival, proliferation, and/or growth of osteoblasts. Therefore, it may be useful in influencing bone mass in such conditions as osteoporosis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:88 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1625 of SEQ ID NO:88, b is an integer of 15

to 1639, where both a and b correspond to the positions of nucleotide residues shown

25 -

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 79

in SEQ ID NO:88, and where b is greater than or equal to a + 14.

The gene encoding the disclosed cDNA is thought to reside on chromosome 17. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 17. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: ARGKYESAQPGGTQPEPGLGAR (SEQ ID NO:617). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in pituitary, cerebellum and kidney and to a lesser extent in a range of fetal tissues including lung, heart and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, metabolic, neurological, and renal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine, renal and nervous systems expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., kidney, fetal, brain, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEO ID NO:203 as residues: Pro-29 to Gly-34, Gln-79 to Arg-84, Arg-146 to Arg-152, Ser-183 to Ser-193, Gly-233 to His-241, Tyr-265 to Pro-278, Thr-304 to Arg-320, Leu-328 to Gly-333, Glu-385 to Arg-399.

The high expression of a secreted gene in the pituitary indicates a role for this gene or gene product in the treatment/detection of metabolic disorders associated with 20 the endocrine system, such as growth and developmental defects. Expression in the cerebellum indicates a role in the treatment/detection of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. Expression in the kidney indicates a role in the treatment/detection of renal disorders such as kidney failure, Wilms Tumor and kidney stones, as well as nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. .

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEO ID NO:89 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

5

10

15

25

30

35

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1846 of SEQ ID NO:89, b is an integer of 15 to 1860, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:89, and where b is greater than or equal to a + 14.

5

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

The translation product of this gene shares sequence homology with ras-related proteins in rats which is thought to be involved in cellular signaling.

This gene is expressed primarily in T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune system disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:204 as residues: Met-40 to Thr-46, Ala-57 to Glu-64, Ser-85 to Leu-91.

The tissue distribution in immune system tissues indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the gene or protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility

in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Expression of this gene product in T cells also strongly indicates a role for this protein in immune function and immune surveillance. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:90 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 825 of SEQ ID NO:90, b is an integer of 15 to 839, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:90, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

20

25

5

10

15

When tested against U937 Myeloid cell lines, supernatants removed from cells containing this gene activated the GAS assay. Thus, it is likely that this gene activates myeloid cells through the Jak-STAT signal transduction pathway. The gamma activating sequence (GAS) is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

30

35

This gene is expressed primarily in fetal liver, osteoclastoma and neutrophils. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases of the bone, haemopoietic system and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune,

haemopoietic and bone, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, skeletal, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in fetal liver, osteoclastoma and neutrophils indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of diseases of the bone, haemopoietic and immune systems, as well as cancer. Furthermore, elevated levels of expression of this gene product in osteoclastoma indicates that it may play a role in the survival, proliferation, and/or growth of osteoclasts. Therefore, it may be useful in influencing bone mass in such conditions as osteoporosis. More generally, as evidenced by expression in fetal liver/spleen, as well as the biological activity data, this gene may play a role in the survival, proliferation, and/or differentiation of hematopoietic cells in general, and may be of use in the augmentation of the numbers of stem cells and committed progenitors. Expression of this gene product in neutrophils also indicates that it may play a role in mediating responses to infection and controlling immunological responses, such as those that occur during immune surveillance. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:91 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1131 of SEQ ID NO:91, b is an integer of 15 to 1145, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

35

5

10

15

20

25

30

This gene is expressed primarily in endometrial stromal cells.

10

20

25

30

35

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, female infertility. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., reproductive, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:206 as residues: Gln-26 to Asn-51.

The tissue distribution in endometrial cells indicates polynucleotides and polypeptides corresponding to this gene are useful for treating female infertility. The protein product is likely involved in preparation of the endometrium of implantation and could be administered either topically or orally. Alternatively, this gene could be transfected in gene-replacement treatments into the cells of the endometrium and the protein products could be produced. Similarly, these treatments could be performed during artificial insemination for the purpose of increasing the likelyhood of implantation and development of a healthy embryo. In both cases this gene or its gene product could be administered at later stages of pregnancy to promote heathy development of the endometrium. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:92 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2036 of SEQ ID NO:92, b is an integer of 15 to 2050, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:92, and where b is greater than or equal to a + 14.

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 83

The gene encoding the disclosed cDNA is thought to reside on chromosome 19. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 19.

This gene is expressed primarily in tissues of the central nervous system (predominantly the cerebellum) and immune system (predominantly the tonsils).

Nucleic acids of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, disorders of the immune system and CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and neurological system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, neurological, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:207 as residues: Pro-43 to Leu-49, Pro-61 to Gly-66, Ser-71 to Ser-83.

The tissue distribution in the immune system indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the gene or protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne. and psoriasis. In

addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Furthermore, the tissue distribution in the central nervous system 5 indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, 10 including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders. Protein, as well as, antibodies directed against the protein may show utility 15 as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:93 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1159 of SEQ ID NO:93, b is an integer of 15 to 1173, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 84

This gene is expressed primarily in testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive disorders and testes diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the testes, expression of this gene at

35

20

25

significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., testes, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:208 as residues: Lys-28 to His-35, Asn-58 to Gly-64, Thr-80 to Asn-86, Pro-96 to Glu-111, Pro-124 to Phe-133.

10 The tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of testes disorders. Furthermore, the tissue distribution in testes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions concerning proper testicular function (e.g. endocrine function, sperm maturation), as well as cancer. Therefore, this gene product is useful in the treatment of 15 male infertility and/or impotence. This gene product is also useful in assays designed to identify binding agents, as such agents (antagonists) are useful as male contraceptive agents. Similarly, the protein is believed to be useful in the treatment and/or diagnosis of testicular cancer. The testes are also a site of active gene expression of transcripts that may be expressed, particularly at low levels, in other tissues of the body. Therefore, 20 this gene product may be expressed in other specific tissues or organs where it may play related functional roles in other processes, such as hematopoiesis, inflammation, bone formation, and kidney function, to name a few possible target indications. Protein, as well as, antibodies directed against the protein may show utility as a tissue-25 specific marker and/or immunotherapy target for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:94 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 808 of SEQ ID NO:94, b is an integer of 15 to 822, where both a and b correspond to the positions of nucleotide residues shown in

SEQ ID NO:94, and where b is greater than or equal to a + 14.

30

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

This gene is expressed primarily in infant brain, bone marrow and activated T-5 cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental, immune and hematopoetic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, hematopoetic and developmental systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, developmental, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:209 as residues: Asn-23 to Val-37.

Expression in infant brain indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of mental retardation and other developmental disorders in addition to neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. Expression of the gene in bone marrow and in B-cells indicates a role in the treatment and/or detection of immune disorders such as arthritis, asthma, immunodeficiency diseases and leukemia. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:95 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1063 of SEQ ID NO:95, b is an integer of 15 to 1077, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:95, and where b is greater than or equal to a + 14.

5

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

The gene encoding the disclosed cDNA is thought to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: SCGSSRRSAKRSLTLKLIDFSHRI (SEQ ID NO:618). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in infant brain, fetal liver and fetal spleen, and to a lesser extent in macrophages, T-cells, erythroid cells and myeloid progenitor cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neurological, developmental and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune and developmental systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, neurological, developing, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:210 as residues: Val-34 to Leu-48, Val-51 to Gly-67, Lys-74 to Asp-81, Thr-93 to Glu-98, Ser-138 to His-149, Ala-186 to Gln-201, Pro-257 to Arg-271.

Expression in infant brain indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of mental retardation and other developmental disorders in addition to neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons

10

15

25

30

35

Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. Its distribution in fetal liver and fetal spleen indicates that this gene may play a role in the development of the hematopoetic and immune systems and that it may play a role in the treatment/detection of immune system disorders such as leukemia, arthritis and asthma. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:96 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2078 of SEQ ID NO:96, b is an integer of 15 to 2092, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:96, and where b is greater than or equal to a + 14.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 87

This gene is expressed primarily in hippocampus, and to a lesser extent in fetal heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, any of a variety of brain disorders including epilepsy, stroke, palsy, and mood disorders including unipolar and bipolar depression. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., brain, heart, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10

15

20

30

The tissue distribution in hippocampus indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, epilepsy, stroke, palsy, and mood disorders including unipolar and bipolar depression, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:97 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1338 of SEQ ID NO:97, b is an integer of 15 to 1352, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:97, and where b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 88

The translation product of this gene shares sequence homology with a C. elegans protein (coded for by C. elegans cDNA yk112f3.5). The gene encoding the disclosed cDNA is thought to reside on chromosome 3. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 3. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

HYFLRTVSGLSVVPVSLRCCMCPPPCTGPAPATAHSPFDPPALPIQFEYQQA (SEQ ID NO:619), QLEAEIENLSWKVERADSYDRGDLENQMHIAEQRRRT

35 LLKDFHDT (SEQ ID NO:620), VPVSLRCCMCPPPCTGPAPATAHS (SEQ ID NO:621), and/or SWKVERADSYDRGDLENQMHIAEQR (SEQ ID NO:622). Polynucleotides encoding these polypeptides are also encompassed by the invention.

10

15

20

25

30

35

This gene is expressed primarily in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, congenital disorders of the liver and spleen. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, hepatic, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in fetal liver and spleen indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). More generally, as evidenced by expression in fetal liver/spleen, this gene may play a role in the survival, proliferation, and/or differentiation of hematopoietic cells in general, and may be of use in augmentation of the numbers of stem cells and committed progenitors. Expression of this gene product in primary dendritic cells also indicates that it may play a role in mediating responses to infection and controlling immunological responses, such as those that occur during immune surveillance. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:98 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 899 of SEQ ID NO:98, b is an integer of 15 to 913, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:98, and where b is greater than or equal to a + 14.

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 89

5 This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, acute immunological disorders such as inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in neutrophils indicates polynucleotides and polypeptides corresponding to this gene are useful for treating an acute inflammatory response. Furthermore, this gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the gene or protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Expression of this gene product in neutrophils also strongly indicates a role for this protein in immune function and immune surveillance. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEO

ID NO:99 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 707 of SEQ ID NO:99, b is an integer of 15 to 721, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:99, and where b is greater than or equal to a + 14.

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 90

When tested against U937 Myeloid cell lines, supernatants removed from cells containing this gene activated the GAS assay. Thus, it is likely that this gene activates myeloid cells through the Jak-STAT signal transduction pathway. The gamma activating sequence (GAS) is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in fetal liver and fetal spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental and/or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and developmental systems. expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., liver, spleen, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:214 as residues: His-23 to Leu-31, His-33 to Pro-41.

15

20

25

The distribution of this gene in fetal liver and fetal spleen and the biological activity data indicates it may play a role in the development of the immune and hematopoetic systems. It may, therefore, play a role in the treatment and/or detection of immune and/or hematopoetic disorders including leukemia, arthritis and asthma.

Furthermore, this gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the gene or protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:100 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 631 of SEQ ID NO:100, b is an integer of 15 to 645, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:100, and where b is greater than or equal to a + 14.

30 FEATURES OF PROTEIN ENCODED BY GENE NO: 91

This gene is expressed primarily in brain and osteoclastoma to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions which include, but are
not limited to, neurological, bone and reproductive disorders. Similarly, polypeptides

WO 99/31117

5

10

15

20

25

30

35

and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, bone and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., skeletal, brain, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:215 as residues: Phe-47 to Cys-54.

Expression of this gene in brain indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. Furthermore, expression in osteoclastoma indicates a role in the treatment and/or detection of bone damage such as fractures and dislocations. Elevated levels of expression of this gene product in osteoclastoma indicates that it may play a role in the survival, proliferation, and/or growth of osteoclasts. Therefore, it may be useful in influencing bone mass in such conditions as osteoporosis. Expression in the placenta indicates a role in the treatment and/or detection of pregnancy disorders such as miscarriage, birth defects, premature birth, in addition to disorders such as placenta previa and placentitis. Specific expression within the placenta indicates that this gene product may play a role in the proper establishment and maintenance of placental function. Alternately, this gene product may be produced by the placenta and then transported to the embryo, where it may play a crucial role in the development and/or survival of the developing embryo or fetus. Expression of this gene product in a vascular-rich tissue such as the placenta also indicates that this gene product may be produced more generally in endothelial cells or within the circulation. In such instances, it may play more generalized roles in vascular function, such as in angiogenesis. It may also be produced in the vasculature and have effects on other cells within the circulation, such as hematopoietic cells. It may serve to promote the proliferation, survival, activation, and/or differentiation of hematopoietic cells, as well as other cells throughout the body. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

10

15

20

25

30

35

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:101 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 549 of SEQ ID NO:101, b is an integer of 15 to 563, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:101, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 92

This gene is expressed primarily in T-cells, bone marrow, fetal liver/spleen and and to a lesser extent in adipocytes, kidney, melanocytes and stimulated fibroblasts.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoeitic disease characterized by alterations in T cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in immune tissues indicates polynucleotides and polypeptides corresponding to this gene are useful for treating autoimmune diseases or proliferative disorders of the developing immune system. This gene product is primarily expressed in hematopoietic cells and tissues, suggesting that it plays a role in the survival, proliferation, and/or differentiation of hematopoietic lineages. This is particularly supported by the expression of this gene product in fetal liver and bone marrow, the two primary sites of definitive hematopoiesis. Expression of this gene product in T cells also strongly indicates a role for this protein in immune function and

immune surveillance. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:102 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1310 of SEQ ID NO:102, b is an integer of 15 to 1324, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:102, and where b is greater than or equal to a + 14.

15

20

25

30

35

10

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 93

The gene encoding the disclosed cDNA is thought to reside on chromosome 4. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 4.

This gene is expressed primarily in fetal tissues including fetal liver/spleen and to a lesser extent in lung, bone marrow, adrenal gland tumor and in the Ntera2 cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adrenal gland or lungs, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., developing tissues, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in fetal and developing tissues indicates polynucleotides and polypeptides corresponding to this gene are useful for treating tumors formed by

poorly differentiated cells, as well as tumors of other tissues where expression has been observed. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:103 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1717 of SEQ ID NO:103, b is an integer of 15 to 1731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:103, and where b is greater than or equal to a + 14.

15

20

25

30

35

10

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 94

This gene is expressed primarily in the prostate derived cell line PC3 and fetal liver/spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, prostatic hypertrophy or prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the glandular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., prostate, immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:218 as residues: Leu-26 to Ser-33.

The tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the prostate including prostatic tumors or benign prostatic hypertrophy. Protein, as well as, antibodies

WO 99/31117 PCT/US98/27059

149

directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:104 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1452 of SEQ ID NO:104, b is an integer of 15 to 1466, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:104, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 95

This gene is expressed primarily in small intestine, and to a lesser extent in breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases of the small intestine. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the small intestine, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., small intestine, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:219 as residues: Glu-37 to Gly-45.

The tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of diseases involving the small intestine, such as cancer of the small intestine or other tissues where expression has been indicated. Protein, as well as, antibodies directed against the

5

10

20

25

30

35

20

25

30

protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:105 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1289 of SEQ ID NO:105, b is an integer of 15 to 1303, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:105, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 96

This gene is expressed primarily in fast-growing tissues such as tumor and fetal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, growth disorders such as tumorigenesis and growth retardation.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fast-growing tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., rapidly proliferating cells, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:220 as residues: Phe-32 to Cys-37.

The tissue distribution in rapidly-proliferating tissues and cells indicates

polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of growth disorders. Furthermore, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are

useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus, this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:106 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1502 of SEQ ID NO:106, b is an integer of 15 to 1516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:106, and where b is greater than or equal to a + 14.

20

25

30

35

15

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 97

When tested against Jurkat T-cells and U937 Myeloid cell lines, supernatants removed from cells containing this gene activated the GAS assay. Thus, it is likely that this gene activates both T-cells and myeloid cells through the Jak-STAT signal transduction pathway. The gamma activating sequence (GAS) is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in placenta, and to a lesser extent in the endometrium.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, pregnancy disorders. Similarly, polypeptides and antibodies directed to

10

15

20

25

30

35

these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the female reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., placental, reproductive, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Expression of this gene in the placenta and endometrium indicates a role in the treatment and/or detection of pregnancy disorders such as miscarriage, birth defects, premature birth, in addition to disorders such as endometriosis, placenta previa and placentitis. Furthermore, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the placenta. Specific expression within the placenta indicates that this gene product may play a role in the proper establishment and maintenance of placental function. Alternately, this gene product may be produced by the placenta and then transported to the embryo, where it may play a crucial role in the development and/or survival of the developing embryo or fetus. Expression of this gene product in a vascular-rich tissue such as the placenta also indicates that this gene product may be produced more generally in endothelial cells or within the circulation. In such instances, it may play more generalized roles in vascular function, such as in angiogenesis. It may also be produced in the vasculature and have effects on other cells within the circulation, such as hematopoietic cells. It may serve to promote the proliferation, survival, activation, and/or differentiation of hematopoietic cells, as well as other cells throughout the body. Alternatively, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for treating female infertility. The protein product is likely involved in preparation of the endometrium of implantation and could be administered either topically or orally. Alternatively, this gene could be transfected in gene-replacement treatments into the cells of the endometrium and the protein products could be produced. Similarly, these treatments could be performed during artificial insemination for the purpose of increasing the likelyhood of implantation and development of a healthy embryo. In both cases this gene or its gene product could be administered at later stages of pregnancy to promote heathy development of the endometrium. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:107 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the 5 scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1675 of SEQ ID NO:107, b is an integer of 15 to 1689, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:107, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 98

15 The gene encoding the disclosed cDNA is thought to reside on chromosome 5. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 5. Recently another group gened and sequenced this gene, calling it MDC-3.13 isoform 1 (Genbank Accession Number: g3860095), which is believed to be a cellular factor involved in the differentiation of dendritic cells. In 20 specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

HEAWLRSAGTREPPREQRTRRRQTAQLALQVPAPSRTPPMATDVFNSKNLAVX AQKKILGKMVSKSIATTLIDDTSSEVLDELYRVTREYTQNKKEAEKIIKNLIKTVI KLAILYRNNQFNQDELALMEKFKKKVHQLAMTVVSFHQVDYTFDRNVLSRLL

25 NECREMLHQIIQRHLTAKSHGRVNNVFDHFSDCEFLAALYNPFGNFKPHLQKL CDGINKMLDEENI (SEQ ID NO:623), HEAWLRSAGTREPPREQRTRRRQTAQLA LQVPAPSRTPPMATDVFNSKNLAV (SEQ ID NO:624), XAQKKILGKMVSKSIAT TLIDDTSSEVLDELYRVTREYTQNKKEAEKII (SEQ ID NO:625), KNLIKTVIKLA ILYRNNQFNQDELALMEKFKKKVHQLAMTVVSFHQVDYTF (SEQ ID NO:626),

DRNVLSRLLNECREMLHQIIQRHLTAKSHGRVNNVFDHFSDCEFLAALYNPF (SEQ ID NO:627), and/or GNFKPHLQKLCDGINKMLDEENI (SEQ ID NO:628). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in placenta, spleen from CLL patients and various T cell libraries, and to a lesser extent in lung, bone marrow, neutrophil, osteoclastoma, and lymphoma tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

30

35

15

20

25

30

35

biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases of the blood particularly diseases afflicting T cells and tumors of blood cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoeitic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., placental, immune, vascular, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in immune tissues indicates polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the blood including leukemias, lymphomas and diseases that alter T-cell function or proliferation. Furthermore, the tissue distribution in placenta indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the placenta. Specific expression within the placenta indicates that this gene product may play a role in the proper establishment and maintenance of placental function. Alternately, this gene product may be produced by the placenta and then transported to the embryo, where it may play a crucial role in the development and/or survival of the developing embryo or fetus. Expression of this gene product in a vascular-rich tissue such as the placenta also indicates that this gene product may be produced more generally in endothelial cells or within the circulation. In such instances, it may play more generalized roles in vascular function, such as in angiogenesis. It may also be produced in the vasculature and have effects on other cells within the circulation, such as hematopoietic cells. It may serve to promote the proliferation, survival, activation, and/or differentiation of hematopoietic cells, as well as other cells throughout the body. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:108 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1929 of SEQ ID NO:108, b is an integer of 15 to 1943, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:108, and where b is greater than or equal to a + 14.

5

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 99

This gene is expressed primarily in rejected kidney, placenta, and melanocytes. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, acute or chronic renal failure. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., renal, placental, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:223 as residues: Thr-41 to Pro-47.

The tissue distribution in kidney indicates polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the kidney, including renal failure of either an acute or chronic nature, as well as nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:109 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the

scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1580 of SEQ ID NO:109, b is an integer of 15 to 1594, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:109, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 100

10

15

20

25

30

35

5

When tested against U937 Myeloid cell lines, supernatants removed from cells containing this gene activated the GAS assay. Thus, it is likely that this gene activates myeloid cells through the Jak-STAT signal transduction pathway. The gamma activating sequence (GAS) is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in spinal cord, and to a lesser extent in melanocytes and fetal spleen/liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, central nervous system diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., central nervous system, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in spinal cord tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of central nervous system disorders, such as Alzheimers Disease, Parkinsons Disease,

WO 99/31117

Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:110 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1728 of SEQ ID NO:110, b is an integer of 15 to 1742, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:110, and where b is greater than or equal to a + 14.

20

25

30

35

15

5

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 101

This gene is expressed primarily in breast and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, breast related disorders and inflammatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast tissue and dendritic cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., breast, immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

WO 99/31117

The tissue distribution in breast indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of breast related diseases and inflammatory disorders. Furthermore, the tissue distribution in breast indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and intervention of breast tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:111 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1487 of SEQ ID NO:111, b is an integer of 15 to 1501, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:111, and where b is greater than or equal to a + 14.

20

25

30

35

5

10

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 102

When tested against sensory neuron cell lines, supernatants removed from cells containing this gene activated the EGR1 assay. Thus, it is likely that this gene activates neuronal cells through a signal transduction pathway. Early growth response 1 (EGR1) is a promoter associated with certain genes that induces various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

Furthermore, when tested against both Jurkat T-cells and U937 Myeloid cell lines, supernatants removed from cells containing this gene activated the GAS assay. Thus, it is likely that this gene activates both T-cells and myeloid cells through the Jak-STAT signal transduction pathway. The gamma activating sequence (GAS) is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

15

20

25

30

35

This gene is expressed primarily in synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, synovial sarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the synovial sarcoma, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., synovium, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in synovial sarcoma, and the biological activity data, suggest that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of synovial sarcoma. In general, the expression of this gene product in synovium indicates a role in the detection and treatment of disorders and conditions afflicting the skeletal system, in particular osteoporosis as well as disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:112 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 777 of SEQ ID NO:112, b is an integer of 15 to 791, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:112, and where b is greater than or equal to a + 14.

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 103

This gene is expressed primarily in human tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, relating to inflammatory diseases such as tonsilitis, and immune system disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tonsils indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of lymphoid tissue disorders such as tonsilitis. Furthermore, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the gene or protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

10

15

25

30

35

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:113 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1623 of SEQ ID NO:113, b is an integer of 15 to 1637, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:113, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 104

This gene is expressed primarily in activated T-cells and prostate tissue. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, T lymphocytes related diseases and inflammation of the prostate. Similarly, polypeptides and antibodies directed to these polypeptides are useful in 20 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune,

reproductive, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:228 as residues: Arg-24 to Trp-36.

The tissue distribution in immune system tissues and prostate tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune and reproductive disorders. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin,

10

15

the gene or protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Expression of this gene product in T cells also strongly indicates a role for this

protein in immune function and immune surveillance. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:114 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1574 of SEQ ID NO:114, b is an integer of 15 to 1588, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:114, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 105

25

30

35

This gene is expressed primarily in human adult pulmonary tissue and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, relating to the lung, neurological and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the respiratory, nervous, and immune systems expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., pulmonary, immune, nervous, cancerous and wounded tissues) or bodily fluids (e.g.,

10

15

20

25

30

35

serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in pulmonary tissue and infant brain tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment for disorders relating to the pulmonary system, the central nervous system, and the immune system. Furthermore, the tissue distribution in pulmonary tissue and fetal tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of disorders associated with developing lungs, particularly in premature infants where the lungs are the last tissues to develop. The tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and intervention of lung tumors, since the gene may be involved in the regulation of cell division.

Additionally, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep

patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders. Also, this gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by

immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ

ID NO:115 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1912 of SEQ ID NO:115, b is an integer of 15 to 1926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:115, and where b is greater than or equal to a + 14.

10

15

20

30

35

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 106

The translation product of this gene shares sequence homology with the KIAA0132 gene product, and also shares homology to Drosophila melanogaster ring canel protein. The gene encoding the disclosed cDNA is thought to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in infant brain and B-cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, relating to the central nervous system and B cell disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., central nervous system, immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:230 as residues: Thr-31 to Trp-42, Gly-49 to His-54, Gly-68 to Glu-75, Ser-77 to Trp-89, Met-142 to Gly-148.

The tissue distribution in infant brain and B-cell lymphomas indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention for central nervous system and immune

WO 99/31117 PCT/US98/27059

165

disorders. Furthermore, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, 5 dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders. Additionally, this 10 gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the gene or protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or 20 proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:116 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1049 of SEQ ID NO:116, b is an integer of 15 to 1063, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:116, and where b is greater than or equal to a + 14.

25

30

15

10

15

20

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 107

When tested against sensory neuron cell lines, supernatants removed from cells containing this gene activated the EGR1 assay. Thus, it is likely that this gene activates neuronal cells through a signal transduction pathway. Early growth response 1 (EGR1) is a promoter associated with certain genes that induces various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation. The gene encoding the disclosed cDNA is thought to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in human gall bladder.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, relating to gastrointestinal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the gastrointestinal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., gall bladder, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:231 as residues: Pro-45 to Pro-51.

The tissue distribution in gall bladder indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of gastrointestinal disorders. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:117 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of

a-b, where a is any integer between 1 to 1601 of SEQ ID NO:117, b is an integer of 15 to 1615, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:117, and where b is greater than or equal to a + 14.

5

10

15

25

30

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 108

This gene is expressed primarily in human whole brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neurodegenerative diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., brain, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:232 as residues: Gln-58 to Asp-64, His-69 to Pro-76, Leu-101 to Glu-108.

The tissue distribution in brain tissue indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of the central nervous system and endocrine system disorders. Furthermore, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

10

20

25

30

35

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:118 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1207 of SEQ ID NO:118, b is an integer of 15 to 1221, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:118, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 109

The translation product of this gene shares sequence homology with human translation initiation factor eIF3 p40 subunit.

This gene is expressed primarily in human adipose, human fetal spleen, and dentritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, adipose, immune and nerve cell disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., adipose, immune, nervous, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:233 as residues: Asn-27 to Ser-33, Gln-44 to Lys-50.

The tissue distribution fetal liver/spleen and dendritic cells indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune and nerve cell disorders. Furthermore, the tissue distribution in adipose tissue indicates polynucleotides and polypeptides corresponding

10

15

to this gene are useful for the treatment of obesity and other metabolic and endocrine conditions or disorders. Additionally, the protein product of this gene may show utility in ameliorating conditions which occur secondary to aberrant fatty-acid metabolism (e.g. aberrant myelin sheath development), either directly or indirectly. Also, the tissue distribution indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of hematopoietic disorders. This gene product is primarily expressed in hematopoietic cells and tissues, suggesting that it plays a role in the survival, proliferation, and/or differentiation of hematopoietic lineages. This is particularly supported by the expression of this gene product in fetal liver, which is a primary site of definitive hematopoiesis. Expression of this gene product in primary dendritic cells also strongly indicates a role for this protein in immune function and immune surveillance. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:119 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1135 of SEQ ID NO:119, b is an integer of 15 to 1149, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:119, and where b is greater than or equal to a + 14.

25

30

35

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 110

The translation product of this gene shares sequence homology with Ig V-chain, which is thought to be important in immune function. When tested against Jurkat cell lines, supernatants removed from cells containing this gene activated the NF-kB transcription factor. Thus, it is likely that this gene activates Jurkat cells by activating a transcriptional factor found within these cells. Nuclear factor kB is a transcription factor activated by a wide variety of agents, leading to cell activation, differentiation, or apoptosis. Reporter constructs utilizing the NF-kB promoter element are used to screen supernatants for such activity.

10

15

20

25

30

This gene is expressed in human synovial sarcoma, infant brain 1NIB cells, macrophages (GM-CSF treated), human endometrial stromal cells-treated with estradiol, human pancreas tumor, hemangiopericytoma, human endometrial tumor, chronic lymphocytic leukemia and a human colon carcinoma (HCC) cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers such as human synovial sarcoma, human pancreas tumor, hemangiopericytoma, human endometrial tumor, chronic lymphocytic leukemia and human colon carcinoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:234 as residues: Leu-21 to Ala-30, Ser-38 to Asp-47, Pro-87 to Asp-94, Leu-197 to Thr-204, Pro-256 to Ser-262, Thr-277 to Arg-282, Thr-293 to Trp-303.

The tissue distribution in numerous cancerous tissues, and the homology to Ig V-chain, as well as the biological activity data, indicates polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of cancers, including human synovial sarcoma, human pancreas tumor, hemangiopericytoma, human endometrial tumor, chronic lymphocytic leukemia and human colon carcinoma, as well as other tissues where expression has been demonstrated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:120 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1501 of SEQ ID NO:120. b is an integer of 15

WO 99/31117 PCT/US98/27059

171

to 1515, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:120, and where b is greater than or equal to a + 14.

5

		Last	₹		ORF	352)	157	ì	553	7	207	700	166	8	305	3	010	717
		First AA Last		Se	Portion ORF		i	23	ì	23	ì	0	`	01	`	25	3	25	3
	First Last	₹	Jo			20)	22	1	22	1	×	2	×	2	24	1	24	
L	First	Ą	of	Sig			1	_		_	·	-	•		1	T-	4	-	•
	ΑĄ	SEQ	О	Ö N	>	125		126		127		128		179	ì	130)	131	
S' NT	Jo	First SEQ	AA of		Pep	47		125		99		192		92	1	48		160	
		5' NT	of	Seq. Start	Codon	47		125		99		192		92		48		091	
	5' NT 3' NT	of	Total Clone Clone	Seq.		1271		1451		1809		1472		196		1239		1405	
	5, NT	of	Clone	Seq.		_		-		-		-		-		-		-	
			Total	L	Seq.	1271		1451		2317		1472		9101		1239		1405	
	Z	SEQ	Д	NO:	×	Ξ		12		13		4		15		91		17 1405	
					Vector	Uni-ZAP XR		Uni-ZAP XR		pCMVSport	2.0	pCMVSport	3.0	209463 Uni-ZAP XR		pCMVSport	3.0	Uni-ZAP XR	
		ATCC	Deposit	Nr and	Date	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97
	-			cDNA	Clone ID	НЕССО50		HTLA154		HKABT24		HLWBF94		HFKFF78		HSYBG37		HTHCA77	
				Gene	No.			2		3		4		5		9		7	

		Last	₹			86	·	09	}	247	1	-	}	1/1	ţ	77	<u> </u>	5		[1/3
		AA First AA Last	jo	Sec	_	33		21	<u> </u>	33)	20	2	28	0	20	ì	30	C7	5	67
L	AA First Last					32		20		32		<u></u>	`	77	ì	× ×	ì	7,0	† 7	ç	77
	First	₹		Sig		Ŀ		-		-		-	•	-		1		-	-	-	-
	Ą	First SEQ	A	Ö	>	132		133		134		135	1	136	,	137		138	2	130	5
5° NT	Jo		AA of ID	Signal	Pep	106		195		240		139		31		67		486	2	00	`
		5' NT	of	Start Signal NO:	Codon	901		195		240	_	139		31		19		486))	6	`
	5' NT 3' NT	of	Clone Clone	Seq. Seq.		1534		1233		862		682		770		565		1356		617	
	5° NT	of	Clone	Seq.		_		-		F		-		-		-		-		3	
			Total	LN	Seq.	1534		1233		1090		682		770		565		1356		617	 -
L	Z	SEQ	А	NO:	×	18		61		20		21		22		23		24		25	
					Vector	Uni-ZAP XR		pSport1		pSport1		Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR		pCMVSport	3.0	Uni-ZAP XR	
		ATCC	Deposit	Nr and	Date	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97
				cDNA	Clone ID	HNHEZ51		HFIAX46		HFOXO72		HODDW40		HSAWG42		HBMSK09		HDPAU16		HFEBE12	
				Gene	No.	8		6		10		11		12		13		14		15	

		100	Last	₹	of	_		5	S	87	Į	/2		99		75				99		99
		Eiret A A I con		o	Secreted	Portion	ionio i	40		7		C7		7.7	c	61	C	73		71		72
	AA First I ast	V		ō	Sig	Pen	300	75	0	0	Ç	5 7	;	17	9	0	Ç	77	- 6	7		97
	Fire	AA	<u> </u>	to	Sig	Pen	-	-	-	-	-	7	-	~	-	-	-	4	-		1	 -
	₹	SEO	1	<u> </u>	Ö	>	QV.	<u> </u>	235	1		<u>. </u>	1/2	747	143	}	77	-	77	<u></u>		5
5' NT	of	First SEO			Signal NO:	Pep	. 69	2	88)	80	~~	98	3	87	<u> </u>	70	2	Q.	 P	00	
		5. NT	y		Start	Codon	69	}	88		×6	?	86	3	87		70)	40	2	- E	2
L	5' NT 3' NT	Jo			Sed.		648		1025		1388)	919)	828		581		789		884)
L	5' NT	Jo	7000		Seq.		Ŀ		-		-		-		-		F		-		-	 .
L			Total	_	_	Seq.	648		1025		1388		919	,	828	-	581		789		884	
L	Z	SEQ	=	9	ö N	×	26		121		27		28		29		30		31		32	
						Vector	Uni-ZAP XR		pBluescript		Uni-ZAP XR		Uni-ZAP XR		209463 Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR	<u>-</u>	Uni-ZAP XR	
		ATCC	Deposit	Nr. ond	INT and	Date	209463	11/14/97	209877	05/18/98	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97
				ANGS			HFLNB64		HCESD11		HSAWZ41		HNFJF07		HNGJ057		HE7TM22		HFRBR70		HTHBK35	
				Gene	2	INO.	16		16		17		18		61		20		21		22	

			Last	Ą		ORF	48	?	~~	8	76	2	Ę	1	¥	}	-		ç	2	Ç	771
			First AA Last	of	Sec		22	:	28	3	33))	22	77	20	24	0	61		,	OC.	67
	100	Last	ΑĄ	of	Sig				27	ì .	32	1	-	1	6	;	×	2	Ę		90	07
	<u>;</u>	AA FIISI FAST	₩	of	Sig	Pep	Ŀ		_	•	-	,	-	•	F	•	-	-	-	-	1	-
		{	SEQ	Д	Ö	X	147		148		149	!	150	2	151		152	1	153)	154	
5, NT	, 14. ()		First SEQ	AA of ID	Signal NO:	Pep	57		38		43		202	 	135		2	•	13)	63)
			5' NT	Jo	Start	Codon	57		38		43		202		135		31		2	}	63	}
	5, NT 3, NT		ot	Clone Clone	Seq.		998		1694		1215		1794		1174		1087		438		734	
	, S		of	Clone	Seg.		-		L				-		_		-		F		-	
	<u>-</u>			Total	Z	Seq.	998		1694		1215		1794		1174		1087		438		734	
	Z		SEO	А	ö	×	33	<u>-</u> -	34		35		36	•	37		38		39		40	
					-	Vector	pCMVSport	3.0	pSport1		pBluescript		pBluescript		pBluescript	SK-	Lambda ZAP	Ш	Uni-ZAP XR		Uni-ZAP XR	
		t t	AIC	Deposit	Nr and	Date	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97
						Clone ID	HWABA81		HKGAA73	·*.	HKIYP40		HKMMW74		HLFB127		HLQCW84		HBNAV22		HTEAM34	
					Gene	No.	23		24		25		26		27		28		29		30	

		Last	¥		ORF	4		55)	44		85	3	44		89	3	52	3	56	3
		First AA	Jo	Secreted		36		25	}	18		8	}	20		×.	?	27	ì	25	1
	First Last	Ą	Jo	Sig		35		24		17		17		19		17		96	ì	24	 : i
	First	¥	Jo	Sig	Pep	-				-	_	-		F		-	1	-		-	,
	Ą	SEQ	А	ÖN	≻	155		156		157		158		159		160		191		162	
5° NT	Jo	First	AA of	Start Signal NO:	Pep	09		209		297		114		92		65		253		382	
		5' NT	Jo	Start	Codon	09		209		297		114		92		65		253		382	
	5' NT 3' NT	Jo	Total Clone Clone	Seq.		1346		866		658		566		1277		442		068		737	-
	S' NT	of	Clone	Seq.		I		53		-		-		-		-		215	_	40	
			Total	LZ	Seq.	1346		866	_	658		999		1277		442		890		737	
	Z	SEQ	Д	Ö	×	41		42		43		44		45		46		47	******	48	
					Vector	Uni-ZAP XR		Uni-ZAP XR		pSport1		pCMVSport	2.0	Lambda ZAP	H	Uni-ZAP XR		Lambda ZAP	II	pBluescript	SK-
		ATCC	Deposit	Nr and	Date	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97	209463	11/14/97
				cDNA	Clone ID	HTHDK34		H6BSG32		HCFAD33		HDTEN81		HFXDT43		HNGHQ09		HHGDF16		HJBCG12	
				Gene	No.	31		32		33		34		35		36		37		38	

		Last	AA A	of	ORF	55		47		129		104		76		354		68)	58)
		First AA	Jo	Secreted	Portion	27		36		23		20		22	· — -	22		37		37	
	First Last	Ą	Jo	Sig	Pep	26		35		22		61		21		21		36		36	
	First	₽Ą	Jo	Sig	Pep	-		_		_		_		1		-		-		-	
L	¥¥	SEQ		ÖZ	>	163		164		165		166		167		168		169		170	
S' NT	Jo	First	AA of	Signal NO:	Pep	259		43		174		18		911		212	,	96		115	
		5' NT	Jo	Start	Codon	259		43		174		18		911		212		96		115	
	5' NT 3' NT	Jo	Clone Clone	Seq.		571		356		913		1356		1547		1311		2071		1899	
	5° NT	of	Clone	Seq.		-		_		1		-		-		-		F		-	
			Total	LN	Seq.	571		356		913		1356		1547		1338		2071		1899	
L	LN	SEQ	О	ÖN.	×	49		20		51		52		53		54		55		56	
					Vector	pCMVSport	2.0	pCMVSport	3.0	Uni-ZAP XR		pCMVSport 1		Uni-ZAP XR		pCMVSport	3.0	Uni-ZAP XR		pCMVSport	3.0
		ATCC	Deposit	Nr and	Date	209463	11/14/97	209463	11/14/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97
				cDNA	Clone ID	HOGAW62		HSWBJ74		HGBHR26		HKDBF34		H6EAB28		HLWA022		HAGFH53		HHENQ22	
				Gene	No.	39		40		41		42		43		44		45		46	

		First AA Last	of AA	Secreted of	Portion ORF	26 69		38 78		34 173		18 63		26 42		26 113		24 155		22 88	
	First Last	AA A	of	Sig		25		37		33		17		25		25		23		21	1
		ΑA	of	Sig	Pep	Ŀ		L		<u> </u> -		-		F		F		-		-	
	Ψ¥	First SEQ	А	ÖZ	>	171		172		173		174		175		176		177		178	
5. NT	of		AA of	Signal NO:	Pep	20		41		33		48		384		46		182		140	
		5' NT	Jo	Start	Codon	20		41		33		48		384		- 26		182		140	
	5' NT 3' NT	of	Clone Clone	Seq.		1543		1133		1480		1336		1705		1031	-	1589		1088	
	5' NT	Jo	Clone	Seg.		_				F		-		178		-		-		-	
			Total	Ľ	Seq.	1543		1133		1490		1336		1705		1031		1589		1088	
	Ľ	SEQ		Ö	×	57		58		59		09		61		62		63		64	
					Vector	pBluescript		pBluescript		Uni-ZAP XR		Uni-ZAP XR		ZAP Express		pCMVSport	3.0	Uni-ZAP XR		Uni-ZAP XR	
		ATCC	Deposit	Nr and	Date	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97
				cDNA	Clone ID	HKMLK53		HSKGQ58		HNFEG93		HAIBZ39		HBXFP23		HEQBF32		HETHE81		HFPAC12	
				Gene	No.	47		48		49		20		51		52		53		54	

		Last	₹	of	ORF	196		128		154	·	90	}	47		126)	98	 } }	5.5	<u> </u>
		First AA Last	Jo	S	Portion	19		42		27		19		19		19	A.	26	,	36	2
	First Last	₹	of	Sig		18		41		26		18		81		<u>∞</u>		25		35)
L	First	AA.	of	Sig	Pep	L		F		-				-		-		F		-	•
L	₹	SEQ	Ω	ö	>	179		180		181		182		183		184		185		186)
S' NT	Jo	First SEQ	AA of ID	Signal NO:	Pep	175		130		204		414	· -	34		133		38		251	
		5° NT	of	Start	Codon	175		130		204		414		34		133		38	-	251	
	5' NT 3' NT	Jo	Total Clone Clone	Seq.		1256		1602		938		1585		1676		1344		1474		2012	
	5' NT	Jo	Clone	Seq.		-		-				122		-	-	_		-		130	
			Total	LN	Seq.	1256		1602		938		1585		1676		1344		1474		2012	
	Z	SEQ	А	Ö.	×	65		99		<i>L</i> 9		89		69		70		71		72	
					Vector	pCMVSport	3.0	Lambda ZAP	II	pSport1		pCMVSport	2.0	pBluescript		Uni-ZAP XR		Uni-ZAP XR		Lambda ZAP	II
		ATCC	Deposit	Nr and	Date	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97
				cDNA	Clone ID	<u> НЪРFF39</u>		HFXHD88		HFOXV65		HKADX21		HPZAB47		HAGFE79		HCE1X60		HFXKD36	
				Gene	No.	55		99		57		28		29		09		19		62	

		Last	Ą	Jo	ORF	89		47		50		55		126		69		70		129	
		First AA Last	Jo	Secreted	Portion	22		16		31		29		22		24		61		26	
	Last	AA.	of	Sig	Pep	21		15		30		28		21		23		18		25	
	AA First Last	₹	of	Sig	Pep	-		-		-		_	•	-		_		-		-	
	Ą	SEQ	8	Ö	>-	187		188		189		190		161		192		193		194	
5' NT	Jo	First SEQ	AA of ID	Signal NO:	Pep	77		203		44		153		969		123		100		100	
	•	5° NT	Jo	Start	Codon	77		203		44		153		969		123		100	· · · · · · · · · · · · · · · · · · ·	001	
	5' NT 3' NT	Jo	Total Clone Clone	Seq.		1267		1748		1570		524		1306		1479		1794		1280	
	5° NT	of	Clone	Seq.		_		-		38		_	-			-		_		-	
			Total	L	Seq.	1267		1748		1570		524		1306		1479		1794		1280	
	LN	SEQ		NO:	×	73		74		75		76	_	77		78		62		08	
					Vector	pBluescript		Uni-ZAP XR		pSport1		Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR	
		ATCC	Deposit	Nr and	Date	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97	209511	12/03/97
				cDNA	Clone ID	HBMCU71		HTEIV80		HFIAP16		HODAV86		HTEDF80		HTODJ69		HE6GR02		HAPNY86	
				Gene	No.	63		64		99		99		<i>L</i> 9		89		69		70	

		Last	₩	Jo	ORF	54		79		4		196		123		549		99		488	
		First AA	of	Secreted	Portion	20		17		25		34		21		27		27		23	
	Last	AA	Jo	Sig	Pep	61		91		24		33		20		26		26		22	
	First Last	Ą	Jo	Sig	Рер	_		-		_		-		-		-		-		-	
	¥	SEQ	А	ÖN	╁	195		961		197		198		199		200		236		201	
5' NT	Jo	First	AA of ID	Signal NO:	Рер	368		174		243		97		18		249		185		51	
		5' NT	of	Start	Codon	368		174		243		97		18		249		185		51	
	5' NT 3' NT	Jo	Total Clone Clone	Seq.		974		1955		638		829		1129		2674		2207		1636	
	5' NT	Jo	Clone	Seq.		-		-		-		-		_		59		-		-	
			Total	NT	Seq.	974		1955		638		829		1129		2674		2207		1636	
	N	SEQ	А	ÖN.	×	81		82		83		84		85		98		122		87	
					Vector	Uni-ZAP XR		Uni-ZAP XR		Lambda ZAP	II	pCMVSport	2.0	Uni-ZAP XR	•	Uni-ZAP XR		209551 Uni-ZAP XR		pCMVSport	3.0
		ATCC	Deposit	Nr and	Date	209511	12/03/97	209511	12/03/97	209511	12/03/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97
				cDNA	Clone ID	HTLDR33		HACB161		HMEIK34		HKAAK02		HEPAA46		HFPCX09		HFPCX09		HLWAA88	
				Gene	No.	7.1		72		73		74		75		9/		92		77	

		Last	*		OP E	2 5	211	30	3		399	20	cor	Š	194	ì	90		7/		84
		First AA Last			Secreted	7.2	C 7	00	67	20	07	70	07	30	64	2.1	10	-	<u> </u>	G.	07
	Last	₹			O.B		1	28	0	36	7	25	<u></u>	28	2	30	2	c	0	-	<u> </u>
	AA First Last	Ą	<u>_</u>	_	Pen	-	•	-	4	-	•	-	-	_	•		-	1	-	-	-
		- 0,		Ċ	<u>;</u> >	237	· }	202	2	203	3	238	007	204	-))	205	202	200	7	207))
5' NT	Jo		AA of			1		158)	71	-	89	3	35		0%	<u> </u>	262	707	306	3
		5° NT	Jo	٠.	Codon	35		158		71		89)	35		68	\)	2,42	1	306)
	5' NT 3' NT	Jo	Clone Clone	Seq.		1770		1639		1860		1032	1	839		1145		2050)	1173	
	5' NT	Jo		Seg.		Ŀ		-		2		-				-		174		F	
L			Total	Z		1770		1639		1860		1034		839		1145		2050		1173	
<u> </u>	ĽN	SEQ		ö	×	123		88		68		124		90		16		92		93	
	-				Vector	pCMVSport	3.0	pCMVSport	2.0	Uni-ZAP XR		Uni-ZAP XR		Lambda ZAP	II	Uni-ZAP XR		ZAP Express		pCMVSport	3.0
		ATCC	Deposit	Nr and	Date	209551	12/12/97	209551	12/12/97	209852	05/07/98	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97
				cDNA	Clone ID	HLWAA88		HOHBV89		ннгвү69		HCEFL57		HMEKU83		HOSBY40		НК FB Н 93		HMTAD67	
				Gene	No.	77		78		1.6		6/		80		81		82		83	

			Last	₹			194		41	 F	100	707	1	<u></u>	8,5	2	ξ	7	52	75	,	 c
			First AA	jo	Secreted	Portion	61		27	ì	3.7	4	1,	-	20	2	2,2	77	d	2	0	<u>•</u>
		Last	Ą		Sig		18		26)	1.	-)	20	2	6	`	-		×		1	 `
		AA First Last	Ą		Sig		_		-		-	•	-	-	-	1	-	•	-	•		-
		₽	SEQ	В	NO:	>	208		209		210) I	110	:	212		213) (214	 - 1	215	
	Z	Jo	First SEQ	AA of	Signal NO:	Pep	16		191	-	173		123)	205		344				120	
			5' NT	oţ	Start	Codon	91		161		173		123		205		344		18		120	
		5' NT 3' NT	Jo	Clone Clone	Seq.		822		1077		2092		1352		913		721		645		563	
		5' NT	Jo	Clone	Seq.		-		-		-		-		-		-		-		-	
				Total	Ľ	Seq.	822		1077		2002		1352		913		721		645		563	
L		Z	SEQ	Д	ON	×	94		95		96		16		86		66		100		101	
					-	Vector	Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR		Lambda ZAP	II	Uni-ZAP XR		Uni-ZAP XR		Lambda ZAP	п
			ATCC	Deposit	Nr and	Date	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97
			-			Clone ID	HTEBP77		690063H		HCACV51		HHPB145		нгорн79		HNGFJ67		HEIAC52		HFXKL58	
					Gene	o No	84		85		98		87		88		68		06		16	

ı		ast	₩	of	ORF	36	·	55)	7		× ×	,	44		4		T	4	Ţ	J
\vdash		Last	<u> </u>			1	,	1	,	57	·		`	14		44		1	<u> </u>	77	
		First AA	Jo	Se	Portion	27	j	21	i	20	ì	23	ì	31		18	·	33)	15	}
Ŀ	Last	Ą	of	Sig		26		20		61	<u> </u>	22	}	30		17		32	1	14	
L	First	₹	of	Sig	Pep	_		-				-		-		-		-		-	
	Ą	SEQ		Ö	>	216		217		218		219		220		221		222		223	
S' NT	of	First SEQ	AA of	Signal NO:	Pep	96		104		44		8		991		198		544		29	
		5' NT	Jo	Start	Codon	96		104		44		∞		166		861		544		29	-
	5' NT 3' NT	Jo	Clone Clone	Seq.		1324		1731		1466		1303		1516		1689	· · · · ·	1935		1594	
	5' NT	Jo	Clone	Seq.		-		-		-		-		-		-		280	· · · · ·	-	
			Total	L	Seq.	1324		1731		1466		1303		1516	-	1689		1943		1594	
	LN	SEQ	Д	Ö	×	102		103		104		105		106		107		108		601	
					Vector	pSport1		pSport1		Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR		pCMVSport	3.0	Uni-ZAP XR		pCMVSport	3.0
		ATCC	Deposit	Nr and	Date	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97
				cDNA	Clone ID	HMVAM60		HMVBR22		HPJCW04		HSIDJ81		HSLFU05		HEQAK71		HOSEQ49		HRAAM50	
				Gene	No.	65		93		94		95		96		46		86		66	

L		Last	ΑĄ		ORF	70		57		58)	42		40		4		164	2	۷.	<u> </u>
		First AA	Jo	Se	Portion	20		23		35	1	20		29		18	•	23) 	44	ţ
L	Last	₹	Jo	Sig	Рер	19		22		34		19		28		17		22	1	43	?
	First	ΑA	of	Sig	Pep	_		<u> </u>		_		-				-		-		-	٠.
	Ą	SEQ	<u>a</u>	Ö.	>	224		225		226		227		228		229		230		231	· ì
5' NT	of	First	AA of	Signal NO:	Pep	<u>8</u> =		233		125		107		19		114		41		97	
		5' NT	of	Start	Codon	811		233		125		107		19		114		41		16	
	5' NT 3' NT	of	Clone Clone	Seq.		1742		1501		791		1637		1588		1926		1063		1615	
	5' NT	Jo		Seq.		_		_		-		-		-		-		_		F	
L			Total	N	Seq.	1742	·	1501		791		1637		1588		1926		1063		1615	
	Z	SEQ	А	NO:	×	110		=		112		113		114		1115		911		117	
					Vector	Uni-ZAP XR		pSport1		pCMVSport	3.0	Uni-ZAP XR									
		ATCC	Deposit	Nr and	Date	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97	209551	12/12/97
					Clone ID	HSDFW45		HSLCQ82		HSSFT08		HTOIW31		HTXKQ85		HUFBK08		HAJAW31		HBJEE48	
				Gene	No.	100		101		102		103		104		105		106		107	

		Last	AA	of	ORF	129	771	7.5	1	367	700
		of of 5'NT First SEQ AA AA First AA Last	of	Secreted	Portion ORF	2.1		26	ì	36	
	Last	Ą	jo	Sig	Y Pep Pep	20	·	24		24	- 1
	First	₹	Jo	Sig	Pep]-		-		-	
	of AA First Last	SEQ		Ö	≻	232		233		234	
S' NT	Jo	First	AA of	Signal	Pep	188		368		302	
		5. NT	ID Total Clone Clone of AA of ID of of	Seq. Seq. Start Signal NO: Sig Sig	Codon Pep	188		1 1130 368		302	
	3, NT	of	Clone	Seq.		1 1221		1130		1507	
	5' NT 3' NT	jo	Clone	Seq.		_		-		118	•
			Total	NT	Seg.	118 1221		1149		1515	
	Ϋ́	SEQ	О	ö	×	118		119		120	
					Vector	209551 ZAP Express		209551 pCMVSport 119 1149	3.0	HTPBW79 209511 Uni-ZAP XR 120 1515 118 1507 302	
	_	ATCC	Deposit	Nr and	Date	209551	12/12/97	209551	12/12/97	209511	12/03/97
				cDNA	Clone ID	HBXGH74		HWBDM68			
				Gene	No.	801		109		110	

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

10

15

20

30

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide

sequence or the amino acid sequence, the present invention provides not only the
generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated
amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA
containing a human cDNA of the invention deposited with the ATCC, as set forth in
Table 1. The nucleotide sequence of each deposited clone can readily be determined by
sequencing the deposited clone in accordance with known methods. The predicted
amino acid sequence can then be verified from such deposits. Moreover, the amino
acid sequence of the protein encoded by a particular clone can also be directly
determined by peptide sequencing or by expressing the protein in a suitable host cell
containing the deposited human cDNA, collecting the protein, and determining its
sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

25

30

10

15

20

25

30

35

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, Virus Res. 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, Nucleic Acids Res. 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, supra.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

15

20

25

30

35

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 Polynucleotide and Polypeptide Variants

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown inTable 1, the ORF (open reading frame), or any fragement specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the presence invention can be determined conventionally using known computer programs. A preferred method for determing the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are:

Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization

WO 99/31117

5

10

15

20

25

30

35

Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is becuase the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignement of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query

15

20

30

35

Land Land

amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be determined conventionally using known computer programs. A preferred method for determing the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or Cterminal deletions, not because of internal deletions, a manual correction must be made to the results. This is becuase the FASTDB program does not account for N- and Cterminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the the query 25 sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

10

15

20

25

30

35

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the Nterminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or Ctermini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequnce are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as E. coli).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after

10

15

20

25

30

35

deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

10

15

20

25

30

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

35

Polynucleotide and Polypeptide Fragments

10

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-

25

30

60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

20

25

5

10

15

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).)

30

35

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')2 fragments) which are capable of specifically binding to protein. Fab and F(ab')2 fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

20

25

30

35

5

10

15

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the

polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

5

10

15

20

30

10

15

20

25

30

35

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells:

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

10

15

20

25

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

30 Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat

10

15

polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al.,

"Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides

correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined.

30

10

15

20

25

30

35

First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying

10

15

20

25

30

35

personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

10

15

20

25

30

35

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I, 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

15

20

25

30

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

35 Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the

proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

20

5

10

15

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

30

35

25

A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

15

20

25

30

35

PCT

Alternatively, a polypeptide or polynucle e other cells which can inhibit the hyperrample, by increasing an immune responsities of the hyperproliferative disorder or T-cells, hyperproliferative disorders can be increased by either enhancing an exist wimmune response. Alternatively, decreased of treating hyperproliferative disorder

eles of hyperproliferative disorders that content of the present invention ated in the abdomen, bone, breast, dige ndocrine glands (adrenal, parathyroid, placed and neck, nervous (central and perfort tissue, spleen, thoracic, and urogenitarly, other hyperproliferative disorders case or polypeptide of the present invention tive disorders include, but are not limited erative disorders, paraproteinemias, purpaldenstron's Macroglobulinemia, Gauch erproliferative disease, besides neoplasia

Disease

ypeptide or polynucleotide of the present ous agents. For example, by increasing the proliferation and differentiation of B and d. The immune response may be increased onse, or by initiating a new immune response, or by initiating a new immune response response or by initiating a new immune response response or by initiating a new immune response response response response response response response res

Examples of autoimmune disorders that can be treated or detected by th invention include, but are not limited to: Addison's Disease, hemolytic anemia antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalc glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Scle Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoir Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflamn Guillain-Barre Syndrome, insulin dependent diabetes mellitis, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be use anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompa

A polynucleotide or polypeptide of the present invention may also be use treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Org rejection occurs by host immune cell destruction of the transplanted tissue throu immune response. Similarly, an immune response is also involved in GVHD, this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that i an immune response, particularly the proliferation, differentiation, or chemotax cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may used to modulate inflammation. For example, the polypeptide or polynucleotid inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both and acute conditions, including inflammation associated with infection (e.g., se shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemis reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperac rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory disease, Crohn's disease, or resulting from over production of cytokines (e.g., IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperprol disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect

Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g.,

- Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiollitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps,

 Parainfluenza Rabies, the common cold, Polio, leukemia, Rubella, sexually,
 - Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that
can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter,

- Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Menigococcal), Pasteurellacea Infections (e.g., Actinobacillus, Heamophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis,
- and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme
- Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections.
- A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

10

15

20

25

30

35

A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteocarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue

regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stoke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

15 **Chemotaxis**

5

10

20

25

30

35

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotaxic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotaxic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotaxic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

10

15

20

25

30

35

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

5

10

15

20

25

A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, caricadic rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

30 Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of

10

15

20

25

30

positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type

10

15

20

25

30

35

Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

5

10

15

20

25

30

10

15

20

25

30

35

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

10

15

20

25

30

35

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO: Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

10

15

20

25

30

10

15

20

25

30

35

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

5 Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	Vector Used to Construct Library	Corresponding Deposited Plasmid	
	Lambda Zap	pBluescript (pBS)	
15	Uni-Zap XR	pBluescript (pBS)	
	Zap Express	pBK	
	lafmid BA	plafmid BA	
	pSport1	pSport1	
	pCMVSport 2.0	pCMVSport 2.0	
20	pCMVSport 3.0	pCMVSport 3.0	
	pCR [®] 2.1	pCR [®] 2.1	
	Vectors I ambda Zan (II S. Datant Nos	- ··	

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res.

- 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are 25 commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS.
- The S and K refers to the orientation of the polylinker to the T7 and T3 primer 30 sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

35 Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain

10

15

20

DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.

The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

15

20

25

30

35

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl₂, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is

used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

5

10

15

20

25

30

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprimeTM DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100TM column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHybTM hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions: 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on

15

20

25

30

35

either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

5 Example 5: Bacterial Expression of a Polypeptide

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Ampr), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high

10

15

20

25

30

affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM immidazole. Immidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

35 Example 6: Purification of a Polypeptide from an Inclusion Body

15

20

25

30

The following alternative method can be used to purify a polypeptide expressed in E coli when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the E. coli fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a 10 high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with $0.16\,\mu m$ membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem

10

20

25

30

35

columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A₂₈₀ monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak Drosophila promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring

10

15

20

25

30

35

signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. E. coli HB101 or other suitable E. coli hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μg of a plasmid containing the polynucleotide is co-transfected with 1.0 μg of a commercially available linearized baculovirus DNA ("BaculoGoldTM baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One μg of BaculoGoldTM virus DNA and 5 μg of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μl Lipofectin plus 90 μl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture

10

15

25

30

35

and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μ Ci of ³⁵S-methionine and 5 μ Ci ³⁵S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

20 Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSport 2.0, and pCMVSport 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

10

15

20

25

30

35

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No.209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

10

15

20

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μg of the expression plasmid pC6 is cotransfected with 0.5 μg of the plasmid pSVneo using lipofectin (Felgner et al., supra). The plasmid pSV2-neo contains a dominant selectable marker, the neo gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of metothrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 -200 μM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. 25 These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the 30 polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which 35 outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

10

15

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACTCACACATGCCCACCGTGCC CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAAACC CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT 20 GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAACCCCC 25 ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT GTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA GGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC 30 ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera

WO 99/31117

5

10

15

20

25

30

35

containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

10

15

25

30

35

It will be appreciated that Fab and F(ab')2 and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (Sec, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2 x 10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

WO 99/31117

Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM 15 with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl2 (anhyd); 0.00130 mg/L $CuSO_4$ -5H₂O; 0.050 mg/L of Fe(NO₃)₃-9H₂O; 0.417 mg/L of FeSO₄-7H₃O; 311.80 mg/L of Kcl; 28.64 mg/L of MgCl₃; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO₃; 62.50 mg/L of NaH₂PO₄-H₂0; 71.02 mg/L of Na₂HPO₄: .4320 mg/L of ZnSO₄-7H₂O; .002 mg/L of Arachidonic Acid; 1.022 mg/L of 20 Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml 25 of L-Asparagine-H₂0; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H₂0; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H₂0; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalainine; 40.0 30 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tryrosine-2Na-2H₂0; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 35 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine;

15

20

25

30

35

0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

10

15

20

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proxial region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	Ligand	tyk2	<u>JAKs</u> <u>Jak l</u>	Jak2	Jak3	STATS	GAS(elements) or ISRE
5	IFN family IFN-a/B IFN-g Il-10	+	+ + ?	- + ?	- -	1,2,3 1 1,3	ISRE GAS (IRF1>Lys6>IFP)
10	gp130 family IL-6 (Pleiotrohic) Il-11(Pleiotrohic) OnM(Pleiotrohic)	+ ?	+ + +	+ ? +	? ? ?	1,3 1,3 1,3	GAS (IRF1>Lys6>IFP)
15	LIF(Pleiotrohic) CNTF(Pleiotrohic) G-CSF(Pleiotrohic) IL-12(Pleiotrohic)	? -/+ ? +	+++	+ + ? +	? ? ? +	1,3 1,3 1,3 1,3	
20	g-C family IL-2 (lymphocytes) IL-4 (lymph/myeloid) IL-7 (lymphocytes) IL-9 (lymphocytes) IL-13 (lymphocyte) IL-15	- - - - ?	+ + + +	- - - ? ?	+ + + + ? +	1,3,5 6 5 5 6 5	GAS GAS (IRF1 = IFP >>Ly6)(IgH) GAS GAS GAS GAS
2530	gp140 family IL-3 (myeloid) IL-5 (myeloid) GM-CSF (myeloid)	- - -	- -	+ + +	- -	5 5 5	GAS (IRF1>IFP>>Ly6) GAS GAS
35	Growth hormone fami GH PRL EPO	ly ? ? ?	- +/- -	+ + +	- - -	5 1,3,5 5	GAS(B-CAS>IRF1=IFP>>Ly6)
40	Receptor Tyrosine Kin EGF PDGF CSF-1	nases ? ? ?	+ . + +	+ + +	- - -	1,3 1,3 1,3	GAS (IRF1) GAS (not IRF1)

10

15

20

25

30

35

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an Xhol site. The sequence of the 5' primer is: 5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCCGAAATGATTTCCCCGAAATGATTTCCCCCGAAATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTTCCCCCGAAATGATTT

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

10

15

20

25

30

35

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, Il-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml genticin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

10

15

20

25

30

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1 x 10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assav Identifying Myeloid

35 Activity

15

20

25

30

The following protocol is used to assess mycloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells. Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2x10e⁷ U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heatinactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM Na₂HPO₄.7H₂O, 1 mM MgCl₂, and 675 uM CaCl₂. Incubate at 37°C for 45 min.

Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

These cells are tested by harvesting $1x10^8$ cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of $5x10^5$ cells/ml. Plate 200 ul cells per well in the 96-well plate (or $1x10^5$ cells/well).

Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are
activated through many different signal transduction pathways. One of these genes,
EGR1 (early growth response gene 1), is induced in various tissues and cell types upon

10

15

20

25

30

35

activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6) 5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS

WO 99/31117 PCT/US98/27059

(Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

NF-κB (Nuclear Factor κB) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF-κB regulates the expression of genes involved in immune cell activation, control of apoptosis (NF-κB appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κB is retained in the cytoplasm with I- κB (Inhibitor κB). However, upon stimulation, I- κB is phosphorylated and degraded, causing NF- κB to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κB include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF-kB promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF-kB would be useful in treating diseases. For example, inhibitors of NF-kB could be used to treat those diseases related to the acute or chronic activation of NF-kB, such as rheumatoid arthritis.

5

10

15

20

25

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

15

20

25

30

10

5

Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF-κB/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF-κB/SV40/SEAP cassette is removed from the above NF-κB/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF-κB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF-xB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described

10

15

20

in Example 13. As a positive control, exogenous TNF alpha (0.1,1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense $15 \,\mu l$ of 2.5x dilution buffer into Optiplates containing $35 \,\mu l$ of a supernatant. Seal the plates with a plastic sealer and incubate at 65° C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

· CANADA AND AND AND AND AND AND AND AND AN						
# of plates	Rxn buffer diluent (ml)	CSPD (ml)				
10	60	3				
11	65	3.25				
12	70	3.5				
13	75	3.75				
14	80	4				
15	85	4.25				
16	90	4.5				
17	95	4.75				
18	100	5				
19	105	5.25				
20	110	5.5				
21	115	5.75				
22	120	6				
23	125	6.25				
24	130	6.5				
25	135	6.75				
26	140	7				
27	145	7.25				

28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is

5

10

10

15

20

25

30

35

incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to $2-5\times10^6$ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1×10^6 cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca⁺⁺ concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating

10

15

tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford,MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford,MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na3VO4, 2 mM Na4P2O7 and a cocktail of protease inhibitors (# 1836170) obtained from Boeheringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and

30

WO 99/31117 PCT/US98/27059

PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂₊ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30°C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mm EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavadin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phospotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

25 Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

35

30

5

10

15

10

15

20

25

30

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (lug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30

seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR

10

products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and
propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

25

30

35

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

10

15

20

25

30

35

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate I hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 μ g/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 μ g/kg/hour to about 50 μ g/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracistemally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), bucally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or mirocapsules.

- Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric
- acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008;
- U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is
formulated generally by mixing it at the desired degree of purity, in a unit dosage
injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable
carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations
employed and is compatible with other ingredients of the formulation. For example, the
formulation preferably does not include oxidizing agents and other compounds that are
known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

10

15

20

25

30

35

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

10

15

20

25

30

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days.

After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

10

15

20

25

30

35

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other

WO 99/31117 PCT/US98/27059

260

disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties.

Applicant's or agent's file		International application No.	
	PZ021PCT	international appropriation	unneringed
reterence number	1 20211 01	1	unassigned
TTTGTGTTGTTTGCT			

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

A. The indications made below relate to the microorganism	•				
onpage 172 line	N/A				
B. IDENTIFICATIONOF DEPOSIT	Further deposits are identified on an additional sheet				
Name of depositary institution American Type Culture	Collection				
Address of depositary institution (including postal code and 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	(country)				
Date of deposit	Accession Number				
14 November 1997	209463				
C. ADDITIONAL INDICATIONS (leave blank if not ap)	plicable) This information is continued on an additional sheet				
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)					
	·				
E. SEPARATE FURNISHING OF INDICATIONS	(leave blank if nos applicable)				
The indications listed below will be submitted to the Inter Number of Deposit")	mational Bureau later (specify the general nature of the indications e.g., "Accession				
For receiving Office use only	For International Bureau use only				
This sheet was received with the international application	on This sheet was received by the International Bureau on:				
Authorized officer	Authorized officer				

Applicant's or agent's tile	PZ021PCT	International application No	
reference number	F2021FC1	<u> </u>	unassigned

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

Γ.					· 		
A.			tions made t	pelow relate to the r 174		ferred to in t	•
	ont	page _		174	line		NA
В.	IDI	ENTIFI	CATIONO	OFDEPOSIT			Further deposits are identified on an additional sheet
Na	meo	f deposi	tary institut	ion American T	ype Culture Co	llection	
		,					
			ositary ins rsity Boule	titution (including	postal code and co	untry)	
			•	20110-2209			
			of Ameri				
Da	teof	deposit				Access	ion Number
			1	8 May 1998			209877
_		DITTO	NAL IND	ICA TIONS (
<u>ر</u>	AD.	DITIO	NAL IND	ICATIONS(leav	e blank ij noi applic	able)	This information is continued on an additional sheet
							· •
			•				
D.	DES	SIGNA	TED STA	TES FOR WHI	CH INDICATI	ONS ARE	MADE (if the indications are not for all designated States)
							
E.	SEP	ARAT	EFURNI	SHING OF IND	ICATIONS (leav	e blank if not i	applicable)
The	indi	cations of Depos	listed belo	w will be submitte	ed to the Internati	onal Burea	u later (specify the general nature of the indications e.g., "Accession
		,					
_				ng Office use only		7[For International Bureau use only
X	Thi	s sheet v	vas received	d with the internation	onal application	T	his sheet was received by the International Bureau on:
J	X,	ربيب	در کردن	20			
Aut	noriz	edoffice	er	1_		Author	nzed officer
					_	11	

Applicant's or agent s tile	07004007	International application No	
reference number	PZ021PCT		unassigned

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

Α.	The indications	made below relate to the	microorganism	eferred to in the description
	on page	177	, line	N/A
В.	IDENTIFICAT	TIONOF DEPOSIT		Further deposits are identified on an additional sheet
Na	ame of depositary	institution American	Type Culture C	ollection
		ary institution (including	g posial code and c	ountry)
M	1801 University anassas, Virgir	nia 20110-2209		
Ur	nited States of	America		
Da	te of deposit			Accession Number
		3 December 1997	•	209511
C.	ADDITIONAL	L INDICATIONS (lea	ve blank if not appli	cable) This information is continued on an additional sheet
		••		·
				
D.	DESIGNATE	D STATES FOR WH	ICH INDICATI	IONS ARE MADE (if the indications are not for all designated States)
Ē.	SEPARATE F	URNISHING OF IND	OICATIONS(lea	ve blank if not applicable)
The				tional Bureau later (specify the general nature of the indications e.g., "Accession
ш,	iver of Deposit)			
	. •			
ZI		receiving Office use only eceived with the internati		For International Bureau use only
	الأي	i	onar application	This sheet was received by the International Bureau on:
ut	horized officer	1	· · · · · · · · · · · · · · · · · · ·	Authonzed officer
		•		
				11

Applicant's or agent s tile		International application No.	
reference number	PZ021PCT	The state of the s	unassigned

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

A Their Production of the Control of	
A. The indications made below relate to the microorganism related on page181, line	ferred to in the description N/A
B. IDENTIFICATIONOF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution American Type Culture Co	
Address of depositary institution (including postal code and co. 10801 University Boulevard	untry)
Manassas, Virginia 20110-2209 United States of America	
States of America	
Date of deposit	Accession Number
12 December 1997	209551
C. ADDITIONAL INDICATIONS (leave blank if not applice	This information is continued on an additional sheet
D. DESIGNATED CT. MICE.	
BESIGNATED STATES FOR WHICH INDICATIO	ONS ARE MADE (if the indications are not for all designated States)
SEPARATE FURNISHING OF INDICATIONS (leave	e blank if not applicable)
	onal Bureau later (specify the general nature of the indications e.g., "Accession
, - ,	
For receiving Office use only This sheet was received with the	For International Bureau use only
This sheet was received with the international application	This sheet was received by the International Bureau on:
uthorized officer	Authonzed officer
	Administration
·	

Applicant a constatile		t leternational application No.	
Applicants or agent's file	PZ021PCT	International application No	unassigned

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

A. The indications made below relate to the microorganism referr	red to in the description
on page, line B. IDENTIFICATIONOF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution American Type Culture College	ction
Address of depositary institution (including postal code and count 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	ry)
Date of deposit	Accession Number
7 May 1998	209852
C. ADDITIONAL INDICATIONS (leave blank if not applicable	e) This information is continued on an additional sheet
	· ·
D. DESIGNATED STATES FOR WHICH INDICATION	NS ARE MADE (if the indications are not for all designated States)
E CEDADATE EUDNICHINIC OF INDICATIONS (L	
E. SEPARATE FURNISHING OF INDICATIONS (leave be The indications listed below will be submitted to the Internation Number of Deposit")	
	-
This sheet was received with the international application Authorized officer	For International Bureau use only This sheet was received by the International Bureau on: Authorized officer
Authorized officer 3	Authorized officer

What Is Claimed Is:

- 1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
- (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;
 - (f) a polynucleotide which is a variant of SEQ ID NO:X;
 - (g) a polynucleotide which is an allelic variant of SEQ ID NO:X;
 - (h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
- (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.
- 2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.
- 3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

- 4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.
- 5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
- 6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
- 7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.
- 8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.
 - 9. A recombinant host cell produced by the method of claim 8.
 - 10. The recombinant host cell of claim 9 comprising vector sequences.
- 11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:
- (a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;
- (c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.
- 12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.
- 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.
- 14. A recombinant host cell that expresses the isolated polypeptide of claim 11.
 - 15. A method of making an isolated polypeptide comprising:
- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
 - (b) recovering said polypeptide.
 - 16. The polypeptide produced by claim 15.
- 17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.
- 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
- (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.
- 19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
- (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

- 20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:
 - (a) contacting the polypeptide of claim 11 with a binding partner; and
- (b) determining whether the binding partner effects an activity of the polypeptide.
 - 21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.
- 22. A method of identifying an activity in a biological assay, wherein the method comprises:
 - (a) expressing SEQ ID NO:X in a cell;
 - (b) isolating the supernatant;
 - (c) detecting an activity in a biological assay; and
 - (d) identifying the protein in the supernatant having the activity.
 - 23. The product produced by the method of claim 20.

```
<110> Human Genome Sciences, Inc. et al
```

- <120> 110 Human Secreted Proteins
- <130> PZ021PCT
- <140> PCT/US98/27059
- <141> 1998-12-17
- <150> 60/068,008
- <151> 1998-12-18
- <150> 60/068,054
- <151> 1998-12-18
- <150> 60/068,064
- <151> 1998-12-18
- <150> 60/068,053
- <151> 1998-12-18
- <150> 60/068,006
- <151> 1998-12-18
- <150> 60/068,057
- <151> 1998-12-18
- <150> 60/068,007
- <151> 1998-12-18
- <150> 60/070,923
- <151> 1998-12-18
- <150> 60/068,367
- <151> 1998-12-19
- <150> 60/068,369
- <151> 1998-12-19
- <150> 60/068,169
- <151> 1998-12-19
- <150> 60/068,365
- <151> 1998-12-19
- <150> 60/068,368
- <151> 1998-12-19
- <160> 628
- <170> PatentIn Ver. 2.0
- <210> 1
- <211> 733
- <212> DNA

```
<213> Homo sapiens
   <400> 1
   gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg
                                                                            60
   aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga
                                                                           120
   teteceggae teetgaggte acatgegtgg tggtggaegt aagecacgaa gaeeetgagg
                                                                           180
   tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg
                                                                           240
  aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact
                                                                           300
  ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg
                                                                           360
  agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc
                                                                           420
  catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct
                                                                           480
  atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga
                                                                           540
  ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg
                                                                           600
  acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc
                                                                           660
  acaaccacta cacgcagaag agceteteee tgteteeggg taaatgagtg cgacggeege
                                                                          720
  gactctagag gat
                                                                           733
  <210> 2
  <211> 5
  <212> PRT
  <213> Homo sapiens
  <220>
  <221> Site
  <222> (3)
  <223> Xaa equals any of the twenty naturally ocurring L-amino acids
  <400> 2
  Trp Ser Xaa Trp Ser
  <210> 3
  <211> 86
  <212> DNA
 <213> Homo sapiens
  <400> 3
 gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc
                                                                           60
 cccgaaatat ctgccatctc aattag
                                                                           86
<210> 4
 <211> 27
 <212> DNA
 <213> Homo sapiens
 <400> 4
 gcggcaagct ttttgcaaag cctaggc
                                                                          27
 <210> 5
 <211> 271
 <212> DNA
 <213> Homo sapiens
 <400> 5
```

WO 99/3111/			PCT/US9	98/27059
·	3			
ctcgagattt ccccgaaatc tagatti	ccc cgaaatgatt	tccccgaaat	gatttccccq	60
addiatelyc cateteaatt agteage	caac catagtcccc	Cocctaacto	CCCCCatooc	120
geoccaace objectaget cogocca	atto toogcoccat	ggctgactaa	tttttt++++	180
ccacycayay gccgaggccg cctcggc	ctc tgagctattc	cagaagtagt	gaggaggctt	240
ttttggaggc ctaggctttt gcaaaaa	igct t			271
<210> 6				
<211> 32				
<212> DNA				
<213> Homo sapiens				
<400> 6				
gcgctcgagg gatgacagcg atagaac	ccc gg			32
<210> 7				
<211> 31				
<212> DNA				
<213> Homo sapiens				
<400> 7				
gcgaagcttc gcgactcccc ggatccg	act c			
J J J J J J J J J J J J J J J J J J				31
<210> 8				
<211> 12				
<212> DNA				
<213> Homo sapiens				
<400> 8				
ggggactttc cc				12
.210. 0				
<210> 9 <211> 73			•	
<211> 73 <212> DNA				
<213> Homo sapiens				
1213 Homo Saptens				
<400> 9				
gcggcctcga ggggactttc ccggggac	tt tccggggact (tccgggact t	tccatcctd	60
ccatctcaat tag				73
<210> 10				•
<211> 256				
<212> DNA				
<213> Homo sapiens				
<400> 10				
ctcgaggga ctttcccggg gactttccg	ig ggactttccc c	ractttaa t	75	<i>a</i> -
caattagtca gcaaccatag tcccgccc	it aacteedees a	toccacco to	regecatet	60
cagtteegee catteteege cecatgget	g actaatttt t	ttatttato of	accocgee	120
george geotetgage tattecage	a gtagtgagga g	gctttttta as	aggeega Addectado	180
cttttgcaaa aagctt	- 3-3-33- 9	J ga	·yyccrayg	240

WO 99/31117

```
<210> 11
  <211> 1271
  <212> DNA
  <213> Homo sapiens
  <400> 11
  ggggctgggc cctgctcagg tggctctctc cttgcaggga ccggcgatgc tctgcaggct
                                                                            60
  gtgctggctg gtctcgtaca gcttggctgt gctgttgctc ggctgcctgc tcttcctgag
                                                                          120
  gaaggeggee aageeegeag agaeeecaeg geeeaecage etttetgggg eteeeceaae
                                                                          180
  accccgtcac agccggtgtc cacccaacca cacagtgtct agcgcctctc tgtccctgcc
                                                                          240
  tagccgtcac cgtctcttct tgacctatcg tcactgccga aatttctcta tcttgctgga
                                                                          300
  gccttcaggc tgttccaagg ataccttctt gctcctggcc atcaagtcac agcctggtca
                                                                          360
  cgtggagcga cgtgcggcta tccgcagcac gtggggcagg tgggggggatg ggctagggcc
                                                                          420
  ggcactgaag ctggtgttcc tcctaggggt ggcaggatcc gctcccccag cccagctgct
                                                                          480
  ggcctatgag agtagggagt ttgatgacat cctccagtgg gacttcactg aggacttctt
                                                                          540
  caacctgacg ctcaaggagc tgcacctgca gcgctgggtg gtggctgcct gcccccaggc
                                                                          600
  ccatttcatg ctaaagggag atgacgatgt ctttgtccac gtccccaacg tgttagagtt
                                                                          660
  cctggatggc tgggacccag cccaggacct cctggtggga gatgtcatcc gccaagccct
                                                                          720
 gcccaacagg aacactaagg tcaaatactt catcccaccc tcaatgtaca gggccaccca
                                                                          780
 ctacccaccc tatgctggtg ggggaggata tgtcatgtcc agagccacag tgcggcgcct
                                                                          840
 ccaggctatc atggaagatg ctgaactctt ccccattgat gatgtctttg tgggtatgtg
                                                                          900
 cctgaggagg ctggggctga gccctatgca ccatgctggc ttcaagacat ttggaatccg
                                                                          960
 geggeeeetg gaceeettag acceetgeet gtataggggg eteetgetgg tteacegeet
                                                                         1020
 cagececete gagatgtgga ecatgtggge actggtgaca gatgagggge teaagtgtge
                                                                         1080
 agctggcccc ataccccagc gctgaagggt gggttgggca acagcctgag agtggactca
                                                                         1140
 gtgttgattc tctatcgtga tgcgaaattg atgcctgctg ctctacagaa aatgccaact
                                                                        1200
 tggtttttta actcctctca ccctgttagc tctgattaaa aacactgcaa cccaaaaaaa
                                                                        1260
 aaaaaaaaa a
                                                                        1271
 <210> 12
 <211> 1451
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (937)
<223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (965)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (975)
 <223> n equals a,t,g, or c
 <400> 12
gccagttcac tcctcggctg gagacactag gtgtcctgcc cctaatctca ccagagccac
                                                                          60
ctcataaacc ctgcaagctc tgcgaagggc agctgggcac agctgaaagc ccagccacca
                                                                        120
gcccatgtcc tgggtgggac tgggccaggag gggccacctc ctactgctga tcaacccgag
                                                                        180
agccctggct gggatccgtc ttccttcacc aacgggagct ccggccccag ggccctgccc
                                                                        240
acctetgtge acceeacat geageaggga geaccetgea ggaggaactg ggeaccetge
                                                                        300
aggggtctgg tggagacgag gatgctacgg aggcagctgc cccatgggac cagtaagagg
                                                                        360
```

```
gatettgggt gggetteect geagagagga ageceteagg agacaceaca gtaageeatg
  ctggagacct ggaggccagg cccgtcamct ggggagctgg ccactaacag cgggcagaga
                                                                         420
  geeteecagg acagecagea cageceeca caegteegag eccaeeteet cattteeceg
                                                                         480
  cttcccgcgt tcccaagcat gggaggacct gccggacgca gcgcaccaty tytcctaaca
                                                                         540
  gagaccaagt ctgagcttca acgcttgcgc agacgacagg cacgtgcaag cytytcytyt
                                                                         600
  ccagcaggag agcccggagc aggacacagc gaytetttca actgcgtccc gacaaacggt
                                                                         660
  cageceette geteetgeag tttatecaag eteaggagga getttetaaa gagaacacag
                                                                        720
  ggagacaget ggetgecaga gaageagtee tggetetgga aggetecace cagetaacag
                                                                        780
  ggcctgtgac acaggtggca gccagcaaga cccactgcag cggcatggcc ctcacagcct
                                                                        840
  cccctgtccc tgtcctggga gcagccccgg caaagantcc tacccagaac aytccaggtc
                                                                        900
  agganggcag ggccntgarg aargtgarga catcctggar arctgtggcc accaaggtgc
                                                                        960
  tgcacggcct ggaggtctcc acacatctgg gcaaacggaa gctttctggg aggagctggc
                                                                       1020
  teccaggeee tgetetecae gecaececat cacagtegea cacacagaca ggeteccaga
                                                                       1080
  ttgtccaccc tccacaggga gaagtcaggg aggtgggcag gggacggggt cagccaccgg
                                                                       1140
  ctcagcctgt gcacgcccat ccctcccagc agcacccctc tccggcccac ctggctggcc
                                                                       1200
  tgagtctgtg gactggcact gcctgataga actttcagta ccttcagtgc ccaaagggcg
                                                                       1260
 cgacgactag cccttaaaag aggctggagc ccctgaggaa gcgggtcttt aggcaaaacc
                                                                       1320
 1380
 aaaaactcgt a
                                                                       1440
                                                                       1451
 <210> 13
 <211> 2317
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (1419)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (2165)
 <223> n equals a,t,g, or c
<400> 13
cctgcagcta ccgtccgcaa ttcccggtcg acccacgcgt ccgggcgact tgcatcgtct
tcaacatgaa gatagccaca gtgtcagtgc ttctgccctt ggctctttgc ctcatacaag
                                                                        60
atgctgccag taagaatgaa gatcaggaaa tgtgccatga atttcaggca tttatgaaaa
                                                                       120
akggaaaact gttctgtccc caggataaga aattttttca aagtcttgat ggaataatgt
                                                                      180
tcatcaataa atgtgccacg tgcaaaatga tactggaaaa agaagcaaaa tcacagaaga
                                                                      240
gggccaggca tttagcaaga gctcccaagg ctactgcccc aacagagctg aattgtgatg
                                                                      300
attttaaaaa aggagaaaga gatggggatt ttatctgtcc tgattattat gaagctgttt
                                                                      360
gtggcacaga tgggaaaaca tatgacaaca gatgtgcact gtgtgctgag aatgcgaaaa
                                                                      420
ccgggtccca aattggtgta aaaagtgaag gggaatgtaa gagcagtaat ccagagcagg
                                                                      480
atgtatgcag tgcttttcgg ccctttgtta gagatggaag acttggatgc acaagggaaa
                                                                      540
atgatcctgt tcttggtcct gatgggaaga cgcatggcaa taagtgtgca atgtgtgcts
                                                                      600
agctgtyyyw aaaagaagct gaaaatgcca agcgagaggg tgaaactaga attcgacgaa
                                                                      660
atgctgaaaa ggatttttgc aaggaatwtg aaaaacaagt gagaaatgga aggctttttt
                                                                      720
gtacacggga gagtgatcca gtccgtggcc ctgacggcag gatgcatggc aacaaatgtg
                                                                      780
ccctgtgtgc tgaaattttc aagcagcgtt tttcagagga aaacagtaaa acagatcaaa
                                                                      840
atttgggaaa agctgaagaa aaaactaaag ttaaaagaga aattgtgaaa ctctgcagtc
                                                                      900
aatatcaaaa tcaggcaaag aatggaatac ttttctgtac cagagaaaat gaccctattc
                                                                      960
gtggtccaga tgggaaaatg catggcaact tgtgttccat gtgtcaagcc tacttccaag
                                                                     1020
cagaaaatga agaaaagaaa aaggctgaag cacgagctag aaacaaaaga gaatctggaa
                                                                     1080
aagcaacctc atatgcagag ctttgcagtg aatatcgaaa gcttgtgagg aacggaaaac
                                                                     1140
                                                                     1200
```

			_			
ttgcttgcac	cagagagaac	aatcctatcc	agggcccaga	tgggaaagtg	catggcaaca	1260
cctgctccat	gtgtgaggtc	ttcttccaag	cagaagaaga	agaaaagaaa	aagaaggaag	1320
gtwmmtcaag	aaacaaaaga	caatctaaga	gtacagcttc	ctttgwkgag	ttgtgtagtg	1380
aatmccgcaa	atccaggaaa	aacggacggc	ttttttgcnc	cagagagaat	gaccccatcc	1440
agggcccaga	tggaaaaatg	catggcaaca	cctgctccat	gtgtgaggcc	ttctttcaac	1500
aagaagaaag	agcaagagca	aaggctaaaa	gagaagctgc	aaaggaaatc	tgcagtgaat	1560
ttcgggacca	agtgaggaat	ggaacactta	tatgcaccag	ggagcataat	cctgtccgtg	1620
gcccagatgg	caaaatgcat	ggaaacaagt	gtgccatgtg	tgccagtgtg	ttcaaacttg	1680
aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aagggcggcc	gctctagagg	atccctcgag	1740
gggcccaagc	ttacgcgtgc	atgcgacgtc	atagctctct	ccctatagtg	agtcgtatta	1800
taagctaggc	actggccgtc	gttttacaac	gtcgtgactg	ggagatctgc	tagcttggga	1860
tetttgtgaa	ggaaccttac	ttctgtggtg	tgacataatt	ggacaaacta	cctacagaga	1920
tttaaagete	taaggtaaat	ataaaatttt	taagtgtata	atgtgttaaa	ctagctgcat	1980
atgettgetg	cttgagagtt	ttgcttactg	agtatgattt	atgaaaatat	tatacacagg	2040
agctagtgat	tctaattgtt	tgtgtatttt	agattcacag	tcccaaggct	catttcaggc	2100
ccctcagtcc	tcacagtctg	ttcatgatca	taatcagcca	taccacattt	gtagaggktt	2160
tactngcytt	aaaaaacctc	ccacacctcc	ccctgaacck	gaaacataaa	atggaakgca	2220
atggtggtgg	taactggtta	atgcagcctt	aataaatggg	ttaccaaatt	aaaggccaat	2280
aggccatcca	ccmaaaattt	tccacccaaa	ttaaaag			2317
-210- 14						
<210> 14						
<211> 1472						
<212> DNA	:					
<213> Homo	sapiens					
<400> 14						
	ccccct		.			
ttatatata	catagtang	gragerace	tgcggcagca	cagacccagt	gcctacatcc	60
ttgcagatgc	cttctacca	cccatggtge	cctggcacag	cctggacccc	gactcagcgc	120
ccatctgcgc	catcaaccag	cygygetaea	ggtgggctgg	cttcatcgtg	gcagctggct	180
atoccatooc	caccastaga	stattatta	gcctcctctt	ctccctgcca	cgcattgtct	240
angtactat	ageagacage	ctccccccc	aggtgtttgc	ccatgtgcac	ccccggacac	300
tagacetaga	atcactaatt	cagattactet	ggctcctcac	ggccttcctg	gcactgctgc	360
taaccaccaa	tatcattoto	cagilletigl	cccttggcac	actcctggcc	tacacattcg	420
cagccaccag	taccaccacc	cogogococo	agaagtcttc	cccgcccagc	tccccaggcc	480
tagacagtat	acacacatac	accaagcage	agagctcctt	ctcagaccac	ctacagctgg	540
acctgggctt	cttggatgg	tacagggata	caggggagct	gaagecagee	ctgaggccct	600
tattaacete	accetcec	atagggtgg	gagcagtggt	gacttgggcg	cttggcgtta	660
teccacacte	gggttacatc	ctactactac	tgcttgtctt	tatastatt	accetgeace	720
tecttatect	aggaratese	carcaacart	tgctcaccag atcgggaaga	cgccatgttt	ctgctcagcc	780
ttcccctgat	tccacccta	agcatcatca	tcaacatctg	cctactcag	accccatgg	840
atctgacctg	agtacacttc	tocatotage	tgctgatggg	ceteatgetg	aaacttagct	900
atogcatcco	gcatagcaag	dadaaccadc	caccactaca	actigeagig	tatttegget	960
acgtggtatt	CCCCaggggg	acctacac	gggagctgcc	ayyyctgaac	ccacacact	1020
aggcaccagc	acaggagge	ageologyagg	agacagtgca	gyctatgcag	cccccagcc	1080
ctcccacacc	tacttagae	ggccacacyg	agtagctgat	cageceacae	regeceegee	1140
ggcagectag	atttacaaa	ctacacacac	ccagacaagc	tangageeee	cccgttgtg	1200
tccagggggt	gaacttcaaa	tetterere	tggggagtcc	ccaygacctt	aggaccttca	1260
tetacceaga	accttcttct	ttatgatga	tgggccttgg	cragtgctgg	rgccarggac	1320
ggatgggaag	gcccacage	caaccastca	ctccagctac	ttaatta	grageagge	1380
cctactaaca	taaaaaaaaa	aaaaaaaaa	ataataataa	regereggee	agccatgtgg	1440
		uuuuuaaadd	aa			1472

<210> 15 <211> 1016 <212> DNA

```
<213> Homo sapiens
<400> 15
ggcacgaget teegeggeat gattteeace eageeegget ecaceceact egetteettt
                                                                      60
aagatcctgg ctctggagtc ggcagatggg catggcggct gcagtgctgg caatgacatt
                                                                     120
ggcccctacg gtgagcggga cgaccagcaa gtgttcatcc agaaggtggt gcccagtgcc
                                                                     180
agecagetet tegtgegtet eteatetaet gggeageggg tgtgeteegt gegeteegtg
                                                                     240
gacggctcac ccacgacagc cttcacagtg ctggagtgcg agggctcccc ggcggctcgg
                                                                     300
ctctcggccc cggcgctacc tgctcactgg ccaggccaac ggcagcttgg ccatgtggga
                                                                     360
cctaaccacc gccatggacg gcctcggcca ggcccctgca ggtggcctga cggagcaaga
                                                                     420
gctgatggaa cagctggaac actgtgagct ggccccgccg gctcctttca gctccctcat
                                                                     480
ggggctgtct ccccagccc tcaccccgca tctccctcac cagcctccac tcagcctcca
                                                                     540
gcaacacctc cttgtctggc caccgtggga gcccaagccc cccgcaggct gaggcccggc
                                                                     600
gccgtggtgg gggcagcttt gtggaacgct gccaggaact ggtgcggagt gggccagacc
                                                                     660
tecgaeggee acceaeacea geceegtgge cetecagegg teteggeact ceceteacae
                                                                     720
ctcccaagat gaagctcaat gaaacttcct ttttgaacaa cgcagctgcc atgatgcctt
                                                                     780
gggatgccct ggtcctgggg gactcaggtg cctccctgat tcctgtggga accccgggtt
                                                                     840
caggccaggg cctccttgga ataaatggtt attgttacta ggtccccacc ttccctcttt
                                                                     900
tetggaagee aaagteacee teeceaataa agteeteact gecaaaaaaa aaaaaaaaaa
                                                                     960
1016
<210> 16
<211> 1239
<212> DNA
<213> Homo sapiens
<400> 16
cccacgcgtc cgcccacgcg tccgcccacg cgtccggctg cggcgcgatg gcggcggggc
                                                                     60
120
cyaagatgaa ggtggtggag gagcccaacg cgtttggggt gaacaacccg ttcttgcctc
                                                                     180
aggccagtcg cctccaggcc aagagggatc cttcacccgt gtctggaccc gtgcatctct
                                                                     240
tecgaetete gggeaagtge tteageetgg tggagteeae gtacaagtat gagttetgee
                                                                     300
cgttccacaa cgtgacccag cacgagcaga ccttccgctg gaacgcctac agtgggatcc
                                                                     360
teggeatetg geaegagtgg gagategeea acaacacett caegggeatg tggatgaggg
                                                                     420
acggtgacgc ctgccgttcc cggagccggc agagcaaggt ggagctggcg tgtggaaaaa
                                                                     480
gcaaccggct ggcccatgtg tccgagccga gcacctgcgt ctacgcgctg acgttcgaqa
                                                                    540
ccccctcgt ctgccacccc cacgccttgc tagtgtaccc aaccctgcca gaggccctgc
                                                                     600
ageggeagtg ggaceaggta gageaggace tggeegatga getgateace eeccagggee
                                                                     660
atgagaagtt gctgaggaca ctttttgagg atgctggcta cttaaagacc ccagaagaaa
                                                                    720
atgaacccac ccagctggag ggaggtcctg acagcttggg gtttgagacc ctggaaaact
                                                                    780
gcaggaaggc tcataaagaa ctctcaaagg agatcaaaag gctgaaaggt ttgctcaccc
                                                                    840
agcacggcat cccctacacg aggcccacag aaacttccaa cttggagcac ttgggccacg
                                                                    900
agacgcccag agccaagtct ccagagcagc tgcggggtga cccaggactg cgtgggagtt
                                                                    960
tgtgaccttg tggtgggaga gcagaggtgg acgcggccga gagccctaca gagaagctgg
                                                                   1020
ctggtaggac ccgcagggac cagctgacca ggcttgtgct cagagaagca gacaaaacaa
                                                                   1080
agattcsagg ttttaattaa ttcccatact gataaaaata actccatgaa ttctgtaaac
                                                                   1140
cattgcataa atgctatagt gtaaaaaaat ttaaacaagt gttaacttta aacagttcgc
                                                                   1200
tacaagtaaa tgattataaa tactaaaaaa aaaaaaaaa
                                                                   1239
<210> 17
<211> 1405
<212> DNA
<213> Homo sapiens
```

<220>

```
<221> SITE
<222> (1403)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (1404)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (1405)
<223> n equals a,t,g, or c
<400> 17
gaattcggca cgaggcagct ttggacatgt cgggcctcat agggagcatg gggtgtggaa
                                                                       60
gtggtggccg tgggctcaaa agctggctgc ttagtttacc agctgtgtga tctcaagcag
                                                                      120
atcaccttct tcttcagagc ctcagtttgc ctgtcggtca tgccctgcct ggaggccgtg
                                                                      180
gccttgatcc tgcttatcct gctggttcca gacccacccc ggggagctgc cgagacacag
                                                                      240
ggggaggggg ccgtgggagg cttcaggagc agctggtgtg aggacgtcag atacctgggg
                                                                      300
aaaaactgga gtttcgtgtg gtcgayyctc rgagtgaccg ccatggcctt tgtgactgga
                                                                      360
gccctggggt tctgggcccc caagtttctg ctcgaggcac gcgtggttca cgggctgcag
                                                                      420
cctccctgct tccaggagcc gtgcagcaac cccgacagcc tgatttttgg ggcactgacc
                                                                      480
atcatgaccg gcgtcattgg ggtcatcttg ggggcagaag ctgcgaggag gtacaagaaa
                                                                      540
gtcattccag gagctgagcc cctcatctgc gcctccagcc tgcttgccac agcccctgc
                                                                      600
ctctacctgg ctctcgtcct ggccccgacc accctgctgg cctcctatgt gttcctgggc
                                                                      660
cttggggarc tgcttctgtc ctgcaactgg gcagtggttg ccgacatcct gctgtctgtg
                                                                      720
gtggtgccca gatgccgggg gacggcagaa gcacttcaga tcacggtggk ycacatcctg
                                                                      780
ggaracctgg cagccctatc tcacaggact tatctctagt gtcctgcggg ccargcgccc
                                                                      840
tgactcctat ctgcagcgct tccgcagcct gsarcararc tycctgtgct gcgcctttgt
                                                                      900
categocoty gyggggggct gottootgot gactgogoty tacotygaga gagacyagac
                                                                      960
ccgggcctgg cagmctgtca cagggacccc agacagcaat gatgtggaca gcaatgacct
                                                                     1020
ggagagacaa ggcctgcttt cgggcgytgg cgcctctaca gaggagccct gaggtccctg
                                                                     1080
cetgeacteg teetgeetge aagesteeeg ttggteecea cageageagt geeteggtte
                                                                     1140
ctctttggct gtcctcgggg actccggctg aggcacatct gccacttttg aattcccggc
                                                                     1200
tggagagctg gcaggaccct gtggctgggc tgggaatgga gctgtcagca ctctgcgtgg
                                                                     1260
gaggeetggg cetgtgeetg catecegete aaggetgeee cageetgggg teeceageet
                                                                     1320
ggctgctgct gggccctgra taaayagagg ccagtacaaa gcccatggat tttgggcctg
                                                                     1380
taaaaaaaa aaaaaaaaa aannn
                                                                     1405
<210> 18
<211> 1534
<212> DNA
<213> Homo sapiens
<400> 18
ggcacgagtc aagcaatctg tccacctcag cctcccaaag tgctggaatt acaagcataa
                                                                       60
ccactgcacc tggtaggcat caaattttga atagagaagt taaccatgat gaatcaacac
                                                                      120
ttgcttgaat cgtttggttc tccctcctcc ttgttcattg tctttattct gctcatctgg
                                                                     180
atgttgcaaa gatgtaaaga ttttttcctt tgttgctata gagtagtgct aactccatca
                                                                     240
ttctggcaga agcaccaaca cccagatccc aaaattaagc atcatttgaa gctatactca
                                                                     300
ctgaaataca gttcttctgg gcagaacaac ttcagaaagg acaaacattg gctttctggc
                                                                     360
cacacggaag aggcaaattt aataaaggaa gaatggaagt aatgttcaat atcaccagga
                                                                     420
tagcctacct gaaatttctt agtacaaatg agaagcaatg tggcccatgt ggctgctata
                                                                     480
540
cgcgtgtacc cttaattatc catttaaaaa gctaattatt gctgttagtg gtggtggtgg
                                                                     600
```

```
ttgcatgtat atacgtgttt caaaaccatc tgacacagcc tattcaatgc tttcctctag
                                                                         660
 ttcatacctc tgtactggtt tcctgtgtct gccacagaaa ttgccaccaa ggtagcttaa
                                                                         720
 agtaatggaa atctgctctc tcacttttct ggaggctaca aatctgcaat caaggtgtca
                                                                         780
 acaggecatg etecetetga aggetetgeg gaagaateet ttettgette tteetagttt
                                                                         840
 tgatggttgc tgccaatcct tggcattccc tggcttgtgg ctgcaacact ccaatctctg
                                                                         900
 cctcaatcat cacatgacet teettgtgta teteetttgt gtetetgtgt teaaatattt
                                                                         960
 cttccctttc tcctgtacat ataccagtca ttggatttag ggttctcttg atccagtatg
                                                                        1020
 atcttatctc aactggatta tatcttcaaa gaccttattt gaacgcctta tttccataac
                                                                        1080
 ggtcacattt ccaagtacaa gggttaggac ttaaaacata ccttcttggg ggccacaatt
                                                                        1140
 taacctatta tatcccacta cacagtatat gccatgacag aacctctttc atgagaccaa
                                                                        1200
 catgaaatgt agagtgatat gattetttat gtgateaatg agtatttgea gacaatgetg
                                                                        1260
atgattcccc tgagaatatc atggctccct cccttactta tttagatatc tgttcaggct
                                                                        1320
gggtgctgtg gctcatgcct ataatcccag cactttggga ggggaggaag gtggttcact
                                                                       1380
tgagcccagg agttcaagac cagcttgggc aacatggtga gaccttgttt ttaccaaaaa
                                                                       1440
aaagaaagaa aaatacaaaa aattagctgg gtgtggtggc acatgcctgt agttcctgct
                                                                       1500
acttgggtgg ctggggtggg agaatcatct gagc
                                                                       1534
<210> 19
<211> 1233
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (491)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (493)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (497)
<223> n equals a,t,g, or c
<400> 19
gcagcgtgag ccaccgtgcc tggctggttt ggggattttc atattgcatg tgacagaaaa
                                                                         60
cctatctgta actagctaaa tagccctttc ccctactgcc ccccaaaagg cggggtttat
                                                                        120
tgtatcatct gattcagaaa tctacgctgg gcttggtagt ttggtttcgg gaacatctgg
                                                                        180
attccaggtc tcaaatgaca tcatcgctat tcatttttct ctttctctgg ttctgccctc
                                                                       240
caccacgtat cagctttgtt ctgtgttggc ctcagcccca ttctcaagtt cacattcagc
                                                                       300
atgaaaaggc tgatcacctc ttccagtcac tcaagcaaaa agccccaggt ttgctgcaat
                                                                       360
gggctagaat agtttgactg taatcacatg accacctcta agccaatctc tgtgggccag
                                                                       420
gcaccccagt ggttggttta rgcctggatc ttgtgacaca ctcctgaaca catgactcga
                                                                       480
gggtggggca nangcanatc ctcacacaga actggtgcgt gattccaggt ggctgatcaa
                                                                       540
tcacctgtgt ccactgtggt tgtatcaarg gcgtgtgggt tgtgctgtgc tgggcgtaca
                                                                       600
ctagtgtgtg cattggccag ctcggkktgc cacgttattg gctttgggat gctggttccc
                                                                       660
```

aggagtggcg gtgggaagat tccacctgct ttctatggta ggaaggcagg tcctggggtg

agggtgagcc ccgaggggga ccagtggcca ctgtggcttg acccgcaggc cttgacctga

gcattgcagg catagtttcc tgcccctgta actgccagat cgagacccag tgagacagtg

gtttccgtcg ccagagactg aaatagtgta ttccctgagg acccctgaag aagcttggct

ttgctacgag ccagacgtcc aggtcacaag tctggctggg acccaaggct cagtcccttt

ataatagctg ttgagttcac ggagtgagta caattatgca tccccactga ggctcaagag

gtgaagtcac atagccagtt agtggtagag atggggcttg aacctgggtc ttcctgactc

720

780

840

900

960

1020

```
actcagctac ctttccatag aaatagggac tggaggccgg gcgcagtggc tcatgccttt
                                                                        1140
aatccccagc acgttggaag gccgaagagg gtggatcact tgagggcagg agttcaaaca
                                                                        1200
aaaaaattaa aaaaaaaaa aaaaagggcg gcc
                                                                        1233
<210> 20
<211> 1090
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (4)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (17)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (47)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (1033)
<223> n equals a,t,g, or c
<400> 20
gatntggcga tacattnaca cagaacagta gacatgatac gccaagntta atagactact
                                                                         60
atagggaaag ctgtacgctg cagtaccgtc cggaattccc gggtcgaccc acgcqtccqc
                                                                        120
gcggctcatg cccccagtat cccggtccag ctattccgag gacatcgtgg gctctcggag
                                                                        180
aaggcgacgc agctcctcgg ggagcccacc atccccgcag agcagatgtt cctcttggga
                                                                        240
tggctgttcc cgctctcact cccgcggccg tgagggccmc aggcctcctt ggagtgagtt
                                                                        300
ggacgtgggc gctctttacc cctttagtcg ctctgggtcg cgagggcggc tcccaagatt
                                                                        360
cogcaactac goottogogt cotootggto gacotogtat agtggatato gotaccatog
                                                                        420
tgcactgcta tgcagaagaa cggcagtcag cggaagacta cgagaaggaa gagagccatc
                                                                        480
ggcagaggag gctgaaggag agagagagga ttggggaatt gggagcgcct gaagtgtggg
                                                                        540
ggccgtctcc aaagttccct cagctagatt ctgacgaaca taccccagtt gaggatgaag
                                                                        600
aagaggtaac gcatcagaaa agcagcagtt cagattccaa ctcggaagaa cataggaaam
                                                                        660
agaagaccag tcgttcaaga aacaagaaaa aaagaaagaa taagtcgtct aaaagaaagc
                                                                        720
ataggaaata ttctgatagt gacagtaact cagagtctga cacaaattct gactctgatg
                                                                        780
atgataaaaa gagagttaaa gccaagaaga aaaagaagaa aaagaaacac aaaacaaara
                                                                        840
aaaagaagaa taagaaaacc aaaaaagaat ccagtgactc aagctgtaaa gactcagaag
                                                                        900
aggacttgtc agaagctacc tgggatggag cagccaaatg tggcagatac tatggattta
                                                                        960
atagggccag aagcacctat taatacatac ctcttcaaga tgaaaaacct ttgaagtatg
                                                                       1020
ggccatgctt tgnttcccgg tggaaggtgc agctatggct gagtatgtta aaagctggga
                                                                       1080
agcgattccc
                                                                       1090
<210> 21
<211> 682
<212> DNA
<213> Homo sapiens
```

```
<220>
 <221> SITE
 <222> (624)
 <223> n equals a,t,g, or c
 <400> 21
 gcaaatatta attgccattt actttgaaac ctaaaatggt caagattcca ttttcctcca
                                                                           60
 ggctaataaa taataatttg caatatatag attgtatttt gtctttgaaa cgctgtgagg
                                                                          120
 agatectett aatgtggeat ggtetgette tatgeettge ttetgtgttt ettgagetee
                                                                          180
 gtggagatag gccccctctc ctggcttctc tgcttgagcc acataaaatg ccacttcaca
                                                                          240
 gctcttccct ttgaagcctg atccagtatg catttggagc taattactgc agttgacaca
                                                                          300
 actccatcta aaagcgtcat gaaagattct gtaatcactg ataagaaaat gatcttgcaa
                                                                         360
 attattgctg tgtcctcctt tattgcctct ttaccttaac agtacagttt acaataatgt
                                                                          420
 aaattttttt ctaatctttc aactttaacc ctagaaattg tagatgtttt agcagtggtt
                                                                         480
 atgtgatatt ggcacaacat aactatataa tttgctcaat attgtggtgc atacctgtaa
                                                                         540
 tcccagctgc tcaggagtct gaggcatgag aatcacatga acccaggaga tggaggttgc
                                                                         600
 ggtgagctga gagcgagtca ctgnactcca gccaggacga cagagtgaaa ccctgtctca
                                                                         660
 aaaaaaaaa aaaaaactcg ag
                                                                         682
 <210> 22
 <211> 770
 <212> DNA
 <213> Homo sapiens
 <400> 22
ccaatactcc tttactttct ttgagttaca atgttgcatc tattctgttc acagccccta
                                                                          60
ggreteettt teetgetgat etttetaggt ettgaetete tgeetegttg ettgaeeget
                                                                         120
acceggette agagteeaat aattatattt teaaetttgt eetgtatatg etecaettet
                                                                         180
tggctggaac tctgttcagt ttatttcctg actttgaact atctccacgt agtgccacct
                                                                         240
tgtttcctga tctaaggact gtgcaactcc tctccagtcg gccacatctc tgaccaaggg
                                                                         300
attcagtgaa aactctggtt tctcacctga actttgatct ttaaccccag ctgacactag
                                                                         360
taatggcctt tgtgatcagg ctctgaaaga agactgactt catgtgaacc atgtgagcat
                                                                         420
attgttcata tatccctcaa ggtggatcct tctttctaa aaggcatcta aaaagcaacg
                                                                        480
gaagttettt tgaaaateag aggetgeett tttggtagea gttettteat ttattetgta
                                                                        540
gaggatccag attgagctct ttataaaata ttctcctaca taatgtactg ggatagtcct
                                                                        600
aacaatagta aaccttgatc cacagatcac atgtgccatt ggataaaaat aaataatgca
                                                                        660
ragraactca ataagaccag cctgtttaaa ggagacatca taaaaacctc cattaaaaaa
                                                                        720
aaaaaaaaa aactcgaggg ggggcccgta cccaatcgcc tgtgatgatc
                                                                        770
<210> 23
<211> 565
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (10)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (21)
<223> n equals a,t,g, or c
<220>
```

```
<221> SITE
  <222> (538)
  <223> n equals a,t,g, or c
  <400> 23
 tccccccggn ctggcaggaa nttcgscacg agcagaaagc aaatcagtgg ttttctggag
 tttgacatgg gggtactaac aagggaactt tttggggtgg tgggaatgct gtatattttg
                                                                         60
                                                                        120
 attgtgggga tggttacatg gttggatgca tttgtcaaaa cacacttaat ggtaatgcaa
                                                                       180
 aatgaatata ttttatttta tgtaaattat acctcaaagt tgaatttttt taaaaagttt
 cttttaaaaa gtaaagacat ttgtggtgct tcttgtaaat tttactgctg attatgacct
                                                                       240
 tgtttcttta gatttgactt tccaagtttg aaaagaccag tttaaaaatg acttttgctg
                                                                       300
                                                                       360
 ggcatggtgg catgtgcacg tagtcttacc tactcaggag gctgacgcag gagggtccct
                                                                       420
 tgagcccagg agttggaggc tacagtgagc tatgattatg ccactgcact ccagcttggg
                                                                       480
 540
 cggtacccaa ttcgcccaaa atgga
                                                                       565
 <210> 24
 <211> 1356
 <212> DNA
 <213> Homo sapiens
 <400> 24
 ggtcattaag tcctagtctc attaattgtt ttcaagcttt tcgcctacat tttagactaa
 ccctgcttat tcctgtgaat caagtagtga tctcctgcag cttggaagaa aaaataaggg
                                                                        60
 atgggtaatg taaaaatctg gatcaatata ctggttctgg gcaattatcc tgcaaattct
                                                                       120
 gccaggtaat aaaagtgagt agggtgccca taatccggaa gtttctttgt ttaggaaaat
                                                                       180
 aaaaacaagg aacttcatag acccccccaa aggggaattc tatatcttga caagtaaaat
                                                                       240
 tttagatgga aattatctac aacaccacac ttacggaaat tgctatcctc actctattat
                                                                       300
                                                                       360
 ttgcaaaagg gttatacaca gtagcacctt ctaactgaag tattaaacag agtttccatt
                                                                       420
gctgtcgtat tttgcttaat tattatcctt atagcaggga taatagttac taacaaaaag
                                                                       480
gaagcatgaa agttttacta tcactgagcc tggtaggact ttttattggg tttagtgatg
                                                                      540
cagttttaaa tgaaacatgc cgcttttgga ttaatacctc tagtaaagga aatttacaga
                                                                      600
tacttaaaaa tcaaatccaa attattgata ggctcaggaa aatqccagct tcagcctgag
                                                                      660
tggctacaaa cctctttaat aaattccagt cttcttatgg attggttaac gccttattaa
                                                                      720
gecetetett getfatatgt ettgtattga tatttggaet etgtatatae aatactataa
                                                                      780
ctcgaattgt ttcttctcgc ctagaagcaa tcaaactcca aatggtgctg taaactgaac
                                                                      840
cacacatgga caggccattc ttccgaggac ccttagattg atcccagggg agccctagct
                                                                      900
gctattcccc attcacgccc ttttcagcag gaagtagcca gaaggagtcg ccgcccaaaa
                                                                      960
teceetaaca geagttagtg tggeatetee acaggaagta atgttgtagg agttactaag
                                                                     1020
aaattatttt aggcagatag agaggaaaag gggtccttgg gaagttttca ttttttaaag
                                                                     1080
catctctgga aaagtttctt gtaaagcccc ggctcttaga gccaggctgg caacctttga
                                                                     1140
tatgcaaatg taagccatta gaaaccaggt ccacccaggc caggtgtggt gctcacgcct
gtaatcccaa cactttggga agcctaggca ggtggatcac ctgaggtcag gagttcgaga
                                                                     1200
                                                                     1260
ccagcctggc caacatggtg aaaccccgcc tctaataaaa acacaaaaaa ctaaaaaaaa
                                                                     1320
aaaaaaaaa aaaaaaaa aaaaaaaa aaaaaa
                                                                     1356
<210> 25
<211> 617
<212> DNA
<213> Homo sapiens
<400> 25
ggcacagcac agcctgagat cttggggatc cctcagccta acacccacag acgtcagctg
gtggattccc gctgcatcaa ggcctaccca ctgtctccat gctgggctct ccctgccttc
                                                                      60
tgtggctcct ggccgtgacc ttcttggttc ccagagctca gcccttggcc cctcaagact
                                                                     120
```

```
ttgaagaaga ggaggcagat gagactgaga cggcgtggcc gcctttgccg gctgtcccct
                                                                          240
  gcgactacga ccactgccga cacctgcagg tgccctgcaa ggagctacag agggtcgggc
                                                                          300
  eggeggeetg cetgtgeeca ggayteteca geecegeeca geegeeegae eegeegegea
                                                                          360
  tgggagaagt gcgcattgcg gccgaagagg gccgcgcagt ggtccactgg tgtgccccct
                                                                          420
  teteceeggt cetecaetae tggetgetge tttgggaegg cagegagstg egeagaaggg
  gcccgccgct gaacgctacg gtccgcagag ccgaactgaa ggggctgaag ccagggggca
                                                                          480
                                                                          540
  tttatgtcgt ttgcgtagtg gccgctaacg aggccggggc aagccgcgtg ccccaggctg
                                                                          600
  gaggagaggg cctcgag
                                                                          617
  <210> 26
  <211> 648
  <212> DNA
  <213> Homo sapiens
 <400> 26
 ggcacgaggt gttttaaacc tcagaaacag atttgagtgt ttcagtatta tagaaacagt
 gatgactatt catgetetge tagtetatge etgeaactee aaatgtttgt ggtteagtat
                                                                           60
 ttcccaccta catttctgtt tggtgacatt gctcatttta acaaatatga ccgagtctag
                                                                          120
                                                                         180
 tttttcttta aaaggatagt ttatgagtaa tctttaaaac catttccata ccatctgtat
                                                                         240
 ataaccattt cggtagagaa cacactacac tgaaccctgc tttagagctg tgtgttgagc
 taaaaatata attttttaaa aattgactag caaaatctat ggccacactg agaagccttt
                                                                         300
 gaaaatggca aatacttttc atcaccaatt gcccaattca tctttcttct gcttcctcag
                                                                         360
 cettgtagca aaggetacae agcageeeac agtecacagt etttttggga aaattggeet
                                                                         420
                                                                         480
 gccaccttct ttaagctcag tttatttttg acttactttc tttgctgtag ttatgaacct
                                                                         540
 tggggcatta aaatcccatg gcaaggagca taagagatgt tctcgtagct ctgcgttgtg
                                                                         600
 tgaaatgtcc atcttagttt tgttaaaaaa aaaaaaaaa aaaaaaaaa
                                                                         648
 <210> 27
 <211> 1388
 <212> DNA
 <213> Homo sapiens
 <400> 27
ggcacgaggt aagttgcaag gtacacccac gggtgattta tcactcttac aaagatgata
                                                                          60
actaatgaag accgcatcta gaatgctctt actggagatg gtttacagag catttttaat
catcatactt agatttatat taatatttct tttcaaacta aattattcca aactgtgccc
                                                                        120
                                                                        180
tgagatacca tttggcctca agttcttttc tttcgtctgt attaaggtgc aaataaaaaa
                                                                        240
gactagtagg aaaagaaggc cttatttatg aaggttgtct atagctctga gcttggtagc
                                                                        300
tacataaaat gagtaataac ctaaataagt aaaactaatg aagatctaac tagattactt
                                                                        360
tgcttaatat taacatttta cccgccccc gccgtgaaac atttggcaga tgttctgcag
                                                                        420
gactcatgag gacattggtg gctacagctg cttctggcac tgcccccca accccccagt
                                                                        480
gaggtgaact tetttacaca tecageaage tttagttate ttettetece atttgagata
                                                                        540
actgtggcta caagaatctc agttaaatca gatgtttaaa ttaggtgcca aaaaatctta
                                                                        600
cagacactga actaatactt aaatcaagga acacttcagt tctccataaa atctggtgcc
attttccaaa gaaacagagg atctttgttt cacacccgtg gtactggaat tgcaacagtg
                                                                        660
                                                                        720
aggcattcta gctctcacat gccaatgcga gtggcattca ttcttgctca ctcatttctg
                                                                        780
cttctcattg tcacacttgg aggctctttg ggggtatgtt tcagttgatc tgagaaactg
                                                                        840
ggtgttacca atttactaga gagtttctta aaatgtatct gaaacaaact attaatgggc
                                                                        900
attctgtggt ggtaaaacca ggcaacgcct ccctacacta tctgtccttt cagagctaag
aatctgttat tttgaattgt tcacgaagag tgattctgac tctgcttcag tgcacacttt
                                                                        960
                                                                       1020
acaaaccatc gagcctcatc aaaggagtga gttgagctga ggaattagag taaagaatac
                                                                       1080
aggtatagtg ccgggcgtgg tgctcacgcc tgtaatccca acattttggg aggacaagga
                                                                       1140
gggtggatca cctgaggtca ggagttcgag accagcctga ccaacatgga gaaaccctgt
                                                                      1200
ctttactaaa aatacaaaat tagctggacg tggtggcaca tgcctgtgat cacagctact
                                                                      1260
caggaggctg aggcaggaga atcgcttgaa cccaggaggc ggaggttgtg gtgagccgag
                                                                      1320
```

```
1380
 aaaaaaaa
                                                                    1388
 <210> 28
 <211> 616
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (17)
 <223> n equals a,t,g, or c
<220>
 <221> SITE
 <222> (580)
 <223> n equals a,t,g, or c
<400> 28
cmgctrctra gcaactnagt gggatscccc gggctgcagg aattcggcac gaggagaacg
                                                                     60
gctgcacgtg ggagatgctc cgtggatgtt tgtagaacgc tggcttccgt gtttcctcgt
                                                                    120
tgtggctgtg gtggtgtggg tctttgcctg tggacccgtg gaagacaaag aagacagttt
                                                                    180
tggatggtca agctattttc ttgcttcagg gctccctccc ctgctttttg aagcctcaca
                                                                    240
aaccaggact gtgagggcag gaaggcttgg ggtctttgtg tgctgagcct cattagggtt
                                                                    300
ttaagaacct ccctcctttc atctctagct tacgagaggg atgattcatt atcttccctc
                                                                    360
ctcaggctgc agtagaagca gacagtctct gcctccctgc ttgcctttcc tccctcccat
                                                                    420
tcactgttga ttattgccct caagaataac aggttgccca gctactcgag argcttaagt
                                                                    480
gggaggattg cttgacccca ggagttcgag gctgcagtga gctatgatcg cttcactgcg
                                                                    540
ctatagectg geagacacag agagacecta teteaagean acagacaaac aaaaaaaaa
                                                                    600
aaaaaaaaa ctcgag
                                                                    616
<210> 29
<211> 828
<212> DNA
<213> Homo sapiens
<400> 29
acgagaacac catgctagtg agttcattcc taacagagga gaacttgcat cttgactaag
                                                                    60
cattagtgat ctcaaatcct ctgcttatga tttttaaact tctgatcttc agaatatttt
                                                                   120
tccatgagct agctctggct ttgtgcatct caaaccttgt ttctctccca tggctgtcat
                                                                   180
acttctggtg ccctgagatg cagaatttat ttctacttga tacacacatt tgggtattga
                                                                   240
tgtagggtta gtacagcagg taggttgaga atttctggag cctccctccc tccctttgtt
                                                                   300
ctgacctttc cttagtcata tcatcctaga aagatcttcc ctggcttcgt ctaaaacatg
                                                                   360
420
ccccaacatc ctttcctgtt tacagcccat ctcccctgct agaacacaag ctctgagagg
                                                                   480
tggaaggcct ctattgtggg ttttggcgaa tccccaatct ctagatggtg tctggcatgt
                                                                   540
gatagagatt caacaaacac ttcaacaaat aatgaataaa gttaaatttt tcagagtgca
                                                                   600
atcatgcctc tcccttcctc tgccagggcg gaggctgtgc ctggtttgcg cggcttctgc
                                                                   660
agctccagct ccttgtactg agtctggaga atgatggagc tcagtccatt ttaatcccat
                                                                   720
gaacattaaa tgcgtggatg tgtggatgct gggatggatg gatgacgctc ctagcacggc
                                                                   780
agcttgcagg ggattggcga tttccagtaa ggtgtgctaa gactcgag
                                                                   828
```

<210> 30 <211> 581

```
<212> DNA
  <213> Homo sapiens
  <400> 30
  ggcacgagat tatgggggca gtttccccaa tgctgttctt gtgatagtag ggaattctca
  tgagagctga tggttttaag tgtggcactt cttcacgctc tctctcacct gatgccatgt
                                                                         60
  aagacgtgcc ttgcttccac ttcaccttct gccatgattg taagtttcct gaggcctccc
                                                                        120
  cagccagcca tgtggaactg tgagtcaatt aaaccttttt tgtttataca ttacccagtc
                                                                        180
  tcaggtagta tctttatagc agtgtgagaa tggactaatg cagtctcttt gttagattgc
                                                                        240
  ctatgtttct tgactgtcta ataagatatg actttcagtg atacaaatga tcagagaacc
                                                                        300
  ttgcaaagct gatgtggtgg agagagttca gggagaacca gagtggaaca aaccggagga
                                                                        360
  atgaatatgg tagagtgcaa gtgaatttgc tcctgatttc cagaagcagt tgtcagcaac
                                                                        420
 agagtttacc cttgtatagc attaaaatag tctaggacaa accagaaagt ccataatgtc
                                                                        480
                                                                        540
 ctccagcatt aagagagcac ctcgtgccga attcggcacg a
                                                                        581
 <210> 31
 <211> 789
 <212> DNA
 <213> Homo sapiens
 <400> 31
 ggcacgagcc tccttccaga agttccaggg ttttctttga tggttgccat tctgcttaga
 gaacttccat tagcctttct tttggtgggg tcttctggtg acaaattctg tttcacttcc
                                                                        60
 totgagaatg ttttgctttc cttttcattc ctgaaggaca tttttgctgg atataagaat
                                                                       120
 tctgggttaa tggttctttt cattgtttaa aaaatatttt gtactttcag ctgggctcca
                                                                       180
 tggtttctga tgagaaattc gctgtcattt gacttgttaa tgcacgatag ttaaggcagt
                                                                       240
 ttttgtttag tggcttttga aatgttttgt cttttgtttt ttggagtttg attattgtat
                                                                       300
 gtcttagttt ggatttcttt gggttcatcc tgtttagggt ttgcttacct aagatctgta
                                                                       360
 gatttatgtc tcttgccaaa tttgggaact tttaagccat cattcgtaga gtacagtttc
                                                                       420
 aaccccacct tctttctcct gtcccttcgt gagttcagtg actggagttg ttatagtccc
                                                                       480
 ataggtcccc aagactggtt ttttttttt tttttttt tttttttt ttttgctggg acatttcttt
                                                                       540
 600
 ttcccatccc ttcccgtccc ttcccatctt cggagtctct ccctgtttcc caggctggag
                                                                       660
 tgcaatggac gttctcggct cactgcaacc gccgcctccc tagttcgaat gattcttctg
                                                                       720
                                                                       780
 tctcagcct
                                                                       789
<210> 32
<211> 884
<212> DNA
<213> Homo sapiens
<400> 32
ggcacgagca gaatcagggc actgagctct actgtaagtg tgtatttaat ctccatttt
aatttgaccc atagaaaatt gtctttatag accaaaaatg gtcaaagatg agcaatttca
                                                                       60
tatctattac atgcttagtg ttcactattt tggggcatct tgtttctctc caggttgcgc
                                                                       120
attcatctgt ttttgagttt aaaaccttgt atgtgcttaa gaccaataga tattctcagt
                                                                      180
cactttttag acatttttgt cacctcagtt ttatcagaac tagaaaaatc ttccttaaaa
                                                                      240
acaactgaaa ccttttcttt tgcagtgttt cttttgctaa tgatgaacta atattaacaa
                                                                      300
cttaccttct aataactttg tctttgtaac tcaggtttaa aagcattact ccaccaatct
                                                                      360
cttttattct ccattaaaag atattatttc ctttataatt catttttatt ccttatttgt
                                                                      420
ttagtgeett aagtetgttt etgtacaget tggagaetgt aaettggaaa aatgtagata
                                                                      480
tattcattat atactatctc acttaaatgt gaattctgaa gaagtttttc tgagaaaata
                                                                      540
aattegtett gtttgagtgt teettetetg tetgetgtat tetaceaggg ggacagagga
                                                                      600
aagaagggca gagaaattct ttcctggatt tcatgaaatc actgaggcca gagcaacaga
                                                                      660
tcatttaact tttctttatc ccgtgtatgt attactgaaa aaaatggtac ataatagaat
                                                                      720
                                                                      780
```

ttgagtttat ttttatctga cttcaggtac atagggacac ttcctgttta gcattgaatt gtgcctttca taaagcaaaa aaaaaaaaaa	aaagaactct	840 884
		004
<210> 33		
<211> 866		
<212> DNA		
<213> Homo sapiens		
<400> 33		
ccacgcgtcc gctccaaaca aacaaaaaat gaactttatt tagatatatt	ttacatatga	60
tgaagtattt ttttgatgta gtagtttttc tcaccttctt tttagtcttc	tctttatcca	120
tttttctttc tgatgaagaa ttccctgtga gtaggaccca gaacataggc	ctttgtcatt	180
tcaaccette gttetetgaa taggetgttt attggcaaca ttaactggaa	acattttatg	240
tacagcattg gagteteact etgtegeete ageteactge aaceteegee i	tcctgggttc	300
aagtgatgtg cactgtatga actgtgagag caagcatatc attataacat t gccaagacag ttctgatgga cttttgaaga gggatttttc aaaagcattt a	tggacaatga	360
attaataaaa taaatcctat gatttatggg aaattctgtt ggatcaactt t	actcatcat	420
ttactataaa ggtagcatgc gtaggcatga atcttgataa gacaagattc t	-ggaaactgt	480
ttctgagtgg gtccttatat tctgcagagc tgaaccaggt ggaataggag	agactttag	540 600
gtaacagtca aacacaacat ccaaaattat gttgaatgta gtggtgagag o	ctattccctt	660
taaaactete tettggttet tetgaetgtg teaagaatae tgtatttgtt t	agtactoot	720
ctggtttttt tttttttt tttgaaatgc actccagcct gggcgacaag a	agtgaaactc	780
tgtctgaaaa gaaagaaaga aagaaaaga aagaaaggaa agaaggaagg a	agaaaaaaa	840
agaaaagaaa gaaaaaaaa aaaaaa		866
<210> 34		
<211> 1694		
<212> DNA		
<213> Homo sapiens		
<400> 34		
ccacgcgtcc gggataaact atttatcata aatttaaatg ttgttattgt g	cctttattg	60
cacatttttt ctcatgcctt ttattataaa atatacttgt tttcaccttg t	ttttggtca	120
aatcccagtt actgtccatg taaacatatg gcaacataag aacgtcactt t	ttttatcct	180
gcactgtggc atacctgctc ttacaagaga ttctgctgca cttacatatt c	aaatgatgg	240
cacagttata gagactttat tattcttaat tctttattta gacttaaaca t ctaattaaaa cagttcatat gatgaacttt ataataaaat atatatttt c	tatttgttg	360
atagtggctc atgtctgtaa tcccagcact ccaggagtct gaggcaggcg g	aggccaggc	360
gcccaagagt ttgagaccag cctggacaac atagggaggt cctgtctcca c	accacttga	420
ttaaaaaatt agctaggcat tgtggtgcat tcttgtggtc ccagctactc c	aaaaaccc	480 540
ggtaggagga ccacttgagc cccagaggtc aagggcgcag taagttgtga g	agtgagact	600
ctgtctcaat gataataatc ataatcataa taaagatatg taccccagag to	caagaatgc	660
aataagetgt gagagtgaga ceetgtetea atgatettaa taatagteae aa	ataaagata	720
tatattitige atcagicigi gggiaatiga atgaigatig ciggagiaaa ag	Ctdadcada	780
atggtacagt gctgtactgt acagtacata agaatcagga gaggcagctg to	tttaagccc	840
cagtettatt atgeecattt aateaaggea tgetggetee tgteatgaat ta	attctgatg	900
ttgagtaaaa ctgtcatctt caattcatat cactttcaaa tgttacatta ta	aagagaaat	960
gtaacctggt aagtactaag ttgtagattg ttacagagtc agaaaagttg gactgatattga ttatggtaag tagtctttcc ttgctaaagg aatgccaatt tt		1020
ttataaagca atcattttta cacaaagatg aaaatacaca tgggtcctca ta		1080
tgttatatgt ataggtttaa atatctaatt tggaaaagct agacatataa at	aryctaaaa aaatttta	1140
atcettgeag ctaccaatat caaactatac agttettgtt agtaceteet et	aggitute agggtatt	1200 1260
tggagagggg gcagagaaaa gagctcaaat tcaagttgtt tttatatctg ac	cataatttt	1320
ttaaaattat aagtcaaatg tttgttaagg gaggggattt aagttattaa tt	aaaataan '	1320
atttttagat cttcagattt tacttatcta tcctaccttc cattgttatt ga	gagttggc	1440

```
tgtattttct tttttttta ctccctggcc tgatttaaag atactctgga acattccaga
  ggcactgaat ttatcattct aaaagggcca tgtagtactc ccaggaggca tagagctgag
                                                                          1500
                                                                          1560
  ccactcaatg tgtcttgagg ttccaaaatt ctgattctat gcttttatga acatgtaatt
  tagcagatgt tacctaatag caaaagaaaa tgctatcttt accagaatgc acttaggaaa
                                                                         1620
                                                                         1680
  aaaaaaaaa aaaa
                                                                         1694
  <210> 35
  <211> 1215
  <212> DNA
  <213> Homo sapiens
  <400> 35
  ggcacgaget tttcagtact etcaettatt catgacacag gaatgaceet ttaetcaaaa
  ctcttgtggt tgttcaaagg tgagcttctt tttcccttag tcttagccta tgtgttgctg
                                                                           60
  ttgtatattg ttaccaagtt caactaccta attttgaagc tctttccaaa taagatacaa
                                                                          120
 attaaaaggg gaagcattgc cagtaacagg tccctagaga gcagtgccag cctgcctgca
                                                                          180
 agaaaagagg agaaacttct taaaaagttt taagcctggg caacataagg agattgtttc
                                                                          240
 tatgaaaaat aaaaattagc caggatggtg gtgtacacct gtagtcccag ctactcggga
                                                                          300
 agatgagatt ggaggatcac ttgggcctgg gaggttgagg ctacagtgaa ctgtgattgt
                                                                          360
 gccactgtac tccagtctgg gcgacagtga aatcttgtct aaacaaaaac aatttaactg
                                                                          420
 ggaagcacag tggtccttga ggacatttaa tatcaggaca aagagcctat gaatatatca
                                                                         480
 ctgatgtata taaaccctaa ggcgttaata aaagctaact gtttagtgtt atccatttaa
                                                                         540
 gggaacagga ggaattgcat aacttttaga ttagtcatag tggtgcctaa gggatatgct
                                                                         600
 gtggtatatt tgtatagcca gggcacttag ccttccaacc aatttatata ccatgttctt
                                                                         660
                                                                         720
 caactgtggg tgagatttag cctcaagatt tgatttacta tatgtaagta cattacttga
 tttctataaa gaatctttag tggaagatgt tattctgaat tatttatcaa tatgattaat
                                                                         780
 ccagttagaa attattaatg atcttccttt atactataca taggataact tttaacttgt
                                                                         840
                                                                         900
 cgctacagtt gttgctctga ggatcttaat tttgttactt tctaggctac atgaagctat
 ctttttaaaa agtgtactct tcattttcac tgttattgtg tacttagcat aaaaaactca
                                                                         960
                                                                        1020
 aatctaggcc aggtgcagtg gctcatgcct gtaatcccag cactttggga ggctgaagca
 tgcggatcac ttgagcccag gagttcaaga ccagcctggg caacatggct aatgaacact
                                                                        1080
 aagcatagtt ttgatgtett teatattaaa gaetttetea aattettaaa aaaaaaaaa
                                                                        1140
                                                                        1200
 aaaaaaaaa aaaaa
                                                                        1215
 <210> 36
 <211> 1794
 <212> DNA
 <213> Homo sapiens
<220>
<221> SITE
<222> (1675)
<223> n equals a,t,g, or c
<400> 36
gctcctctag tgactgctgg ggtgctagtt ttcacggtta ccacagaact tgagagagga
aaatgagaac ggcaaattaa aatgccataa aattccattc ttaacaagcg ttagttttt
                                                                         60
tttcctatat atccactccc tcacctatct tatgacatat gagaaatcct aacatgggac
                                                                        120
ttggtgtata attagcattg aatgaattta agttttcttt ctttctttct tttctttat
                                                                        180
                                                                        240
cttctgtggt ctcctgcaga atcagtctat aaaaagggca tggtaaaaaa aaatctatct
catagcattg ttgaaaagat taaatgacat aataagatga tgcatatata gtagctagca
                                                                        300
ctgtacctga tgcatattag gagcttgata atattactaa cattatcatc atcaatgcta
                                                                        360
totgagcaaa gaggotgtto ottotttoca gocagagtto ttotgttgga taatatttoo
                                                                        420
agctgtgaac cccaaccaga gaccttgaag cctttatttc cttttctctc attggccttt
                                                                        480
ggctgaagtc tcctttctgc agagaacaaa gtgaccagct tttgatgaac tattttcctc
                                                                        540
                                                                        600
```

```
ttttatccat ttccaagtgt tagccatagt gaagaagtgt agctgggtgc tagcccaact
                                                                          660
 caagaagtga taatgtwata tccaacccaa gataaactca aggataactt tcaacacggc
                                                                          720
 tactcaagca gttcaggggg gaggcatctt gtagagagga gaccaggaag tcacttggca
                                                                          780
 gctgggccag cacacagagg gccattgctc cagtaaagca gctaacctcc atctcttcat
                                                                          840
 caaaccatcc tagactcagc actctgcaga gaaggagcag atggagggaa tgtgtggaga
                                                                          900
 gattagataa gaaggatttc taatctagtg ggggagcgag taaaatgtac agaagtttga
                                                                          960
 gaagccaagc tcttatgtam maatccrccc ccatcactca acaatcccca ctgtatgaat
                                                                        1020
 aaagcctgga aagtttccaa ttaaaacagt gcttgtgaat attggcaagg ggtatctttg
                                                                        1080
 tgtgcagggt acatttaaag ggagaagggt gaagatacac ccttgcctty taggagtaca
                                                                        1140
 ctttctgaga gcttgttcac caggctgtga gtttctcagt ctatctgttt ctcagtctgt
                                                                        1200
 tagtaatgaa tgtatctccc acttagcaca gcagctagca catagtagat gcctaacaaa
                                                                        1260
 tgtgtgttaa attgaatgtt ggaagtctgt gtcctgaaag cttttcttca catattacaa
                                                                        1320
 ggctttttat ttgttcaaca catttttacc aagttttttt ctgtgttcca ggtcttttga
                                                                        1380
 ttagctgttt ttaagtcaca gaaatgggtg tcgggaacaa aaccagtcaa aagtcctcat
                                                                        1440
 tctacatcat ttacactttc ccttcctata tttataagtt ttaatatcag cttctacaat
                                                                        1500
 aggttccaga acaagtggtg ctcaaggaat ggagaaaatg actattccaa ccctagctgt
                                                                        1560
 aggtgaacca aaaaccccag agaaatcaaa gtgtagttta aagcagtgct tctcaagttg
                                                                        1620
 taatgtgcat atagatcacc tggggttgtt attaaaatgc aaattctaaa agagncagga
                                                                        1680
 gaatatettg ageetgggag ceagaggttg cagtgageeg agateattee actgeattee
                                                                        1740
 ageetgggtg acacagegag actecatett aaaaaaaaaa aaaaaaaact egta
                                                                        1794
 <210> 37
 <211> 1174
 <212> DNA
 <213> Homo sapiens
<400> 37
ggcacgagca aaggcaggaa cttttgtcat ttttgttctt caagatgtcc ccaatgccta
                                                                         60
cagcagtaag tgcactgctg ggcacacagt aggtattcaa taaacattca atgaatgaat
                                                                        120
gaatgaatga atgaatgaat gcattgccaa accttgcatg gctgcctttt gttcctgccc
                                                                        180
tagctgctgc ctccccagcc ggcctggctg ctcccgagag cagagatgtg ccttttcctg
                                                                        240
tgagccctgc cacacagttg aacattgggt agagcccatg ggccaggggc agaggcagga
                                                                        300
acacactcag ggcagcgtgc tgccttcctc ccatccttct agaggcaaag ccaccacagt
                                                                        360
ccattcctgt tgccaagagc cttgggggta ggggaagtag acaggaattc accactcctt
                                                                        420
aaaaccagag aagtccagag tcctctgagg gacagggctc ttgatgttca gagggaatca
                                                                        480
geeteggeet ggggaggetg ggatttgggt ggtttattet teageateea ettettetee
                                                                        540
agggagicig icagigacag gaaaagigac icagaacccc agagccaggc ciagiggaca
                                                                        600
ctaggttctg cctgtcccat ggagggtgct gtggctttga cggattagaa gtcaggactt
                                                                        660
ggccatcatg actacatgct ttaaaaaata tgagttttct ttttttgttt tgggttttt
                                                                        720
aaggeggtgg ggggetaett tgtgtttagg ttttacatee tttgcaataa agttecaeee
                                                                        780
atccagcttg tgcagtgaaa aagagggaaa ggacttcagt ggctttgcct tgtctataca
                                                                        840
tgggccagag agaaaaagg aagagggctg ggcgcggtgg ctcacgcctg tggtcccagt
                                                                        900
actttgggag gccgaggtgg gaggatcacc tgaggtcagt agttgagacc agcctggcca
                                                                        960
acatggcaaa atcccgtctc tactaaaaat acaaaaatta cctgggcgtg gtggtgggca
                                                                      1020
tetgtaatee cagetaetee agaggetgag gegggagaat ggettgaace caggaggeat
                                                                      1080
aggctgccag tgagccgaga tcatcccatg gcactctagc ctaagggata gagtgagact
                                                                      1140
ctgtctcaaa aaaaaaaaa aaaaaaaaaa aaaa
                                                                      1174
<210> 38
<211> 1087
<212> DNA
<213> Homo sapiens
```

<220>

<221> SITE

```
<222> (408)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (1005)
 <223> n equals a,t,g, or c
 <400> 38
 gtccattctt accaccactc tcccaggtaa atgctccatc ttctctgtct tgggttgcat
                                                                        60
 ttggtcccac ctggtcttct ttcagttaac tcccttcagt ccacccaatg cagtctttc
                                                                       120
 tctgcagcca aattttttc tatagttcag gtctgatgat accactttcc attttcaaac
                                                                       180
 teettaaatt ggeeteggag acctgtgatg gecaatette eccaeceetg tgggteaggt
                                                                       240
 tectetggtg tgggeetate tettagtgca aggetecetg tagaetgtee tggggetgee
                                                                       300
 tgtctaattg tcttctcatg aaccaggtag gcargcagga accactcatc tagtctgggg
                                                                       360
 gtgactgggg ggtgcgaaag ttttgttaca ggatgtattt aacacttnca ttgtctggct
                                                                       420
 caaaattctc tttgaagaaa ctgcctttgt ttaattctgt ttawttattt agaacttacc
                                                                       480
 tagaattgat ttgcacttgc aaaaatgctg ctgttttaga gtttgctttc taggctggtt
                                                                       540
 gettgetetg teacettage taaaaactag gtactggagt geetttteta tteyettete
                                                                       600
 ttctttcttt cttcttcttt tttttttktt tttttagtgg agtctggctt tgtcgcccgg
                                                                       660
gcttaagtgc agtggcacga tcccggctca ctgcmtcctc cgcctcccag gakaagccct
                                                                       720
 tgaacctggg agggagttgc ggtgagcgga gatcgggcca ttgcactcca gcccgggcaa
                                                                       780
cagateetga etettateaa aaaaaaaaa aaaagaaaat taacettagt ttaaetttet
                                                                       840
tgctttacca agtttttaat ttttaaaatt ttttactctt ttgtaatagc acttagttta
                                                                       900
aaacacaaca cattgtacag ctgtactaaa tatatcttca tttatatcat tgttccatag
                                                                      960
cttttttctt ttgtgtgtgt gtgtgtgt gtatgtgtgg gtgancagtg agatccgtct
                                                                     1020
1080
caattcg
                                                                     1087
<210> 39
<211> 438
<212> DNA
<213> Homo sapiens
<400> 39
ggcacgaggc aaatgccata tatgtttaga ccagcctttc tcaattgtgg cacttttgcc
                                                                       60
atttttggcc agttaaattc tgttgtgggg gctgtcctgt gcattgcagg atgtttagca
                                                                      120
geatetetgg cetetaceta etaaatgeea gtgeaceete eetgeagtta aatgaceeea
                                                                      180
aatgtctcca gacataggca aatgttcccc ggagaacaaa gtcatctttg gttgaggaac
                                                                      240
aaaatgaacc tatatttaag atggtctaaa tgtttctgag atggtctaaa catttataag
                                                                      300
cttaacaatt aacttgaaac tcttcaggac tagagaagct atttgtaaat ttaaacatct
                                                                      360
gacgccttga aacaccttta tcataaagat aactaaacca gtgttctttg tgaatggcca
                                                                      420
aaaaaaaaa aaaaaaaa
                                                                      438
<210> 40
<211> 734
<212> DNA
<213> Homo sapiens
<400> 40
gctcgtgccg ctgctgggca ctgggagcag ggggcggcca aaggcagtgg gtgggcaggt
                                                                      60
ccatgectee eetggeeece cagetetgea gggeagtgtt cetggtteet atettgetge
                                                                     120
tgctgcaggt gaagcctctg aacgggagcc caggccccaa agatgggagc cagacagaga
                                                                     180
aaacgccctc tgcagaccag aatcaagaac agttcgaaga gcactttgtg gcctcctcag
                                                                     240
tgggtgagat gtggcaggtg gtggacatgg cccagcagga agaagaccag tcgtccaaga
                                                                     300
```

```
eggeagetgt teacaageae tettteeace teagettetg etttagtetg gecagtgtea
                                                                       360
 tggttttctc aggagggcca ttgaggcgga cattcccaaa tatccaactc tgcttcatgc
                                                                       420
 teacteactg accetecete cetectggge tecaggteac aacteecaaa ggagatgeag
                                                                       480
 gcatggctct ctgcctctga tcaccatcac tgtatctcaa ggttcagcag cagagatacc
                                                                       540
 agttgccatc agtgctaact gactgcctct ccaggttcgg agtttcatct cccagggcca
                                                                       600
 gagacagcag acccacatcc ttctcccca cacctctcct ggttttgttc aggacagcag
                                                                       660
 attagaggca ggaggcaatg acaataaaat aacgataaaa teetgagaac aaaaaaaaaa
                                                                       720
 aaaaaaact cgag
                                                                       734
 <210> 41
 <211> 1346
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (707)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (998)
 <223> n equals a,t,g, or c
 <400> 41
gggcagmgya aacacctctt cttataaaca tggccctgct ttagcaacag gtctccatta
                                                                       60
tgaagcaatt tggatttgga catcctatca agttacttaa aactaaactc tgccgtatag
                                                                      120
tgttttactt ggtatttttt gtgtggccac agtctagtgt gatcagagaa gccacacaga
                                                                      180
cataaattcc cagtcctgat tccattgatt attagatatg tacttaccct gaacatctgt
                                                                      240
aagatgggga gtaatgatgt ttaccacaaa gagttagtgt aaggattcga tgagagaact
                                                                      300
tgcatttgag ccatctggag agaatgttag ttttagcact aacgatcgtt tataatactg
                                                                      360
ctgaggagga aggactgaca tcaccctgct tgagaatcta gtatatgttg ggcattccyt
                                                                      420
atccattcat gagcctgaga gtacttgaga wgttttgatc ttggacactg ytgtgcagct
                                                                      480
ttaaggatga tgagggggaa atggaaagag tcytgaaggg accagtgtca gagacagata
                                                                      540
gaaaagggct gcctgagccg ggcgcagtga ctcacgcctg taatcccaac actttgggag
                                                                      600
gccggggcgg gtggatcacc tgaggtcggg agttcgagac ccgtctaacc aacatggaga
                                                                      660
aaccctgctt ctactawaaa tacaaaatta gccaggtatg gtggcanatg cctgttaccc
                                                                     720
cagctgcttg ggaggctgag gcaggagaat tgcttgagag gcagaggttg ttgtaagccg
                                                                      780
agwtcgcgcc attgcacgcc agcctgggca acaagatkga aactcccatc tcaaaaaaag
                                                                      840
aaaagaaaag ggctgcctgg gtccctggga agacccagct cccctctgta tcctagccaa
                                                                      900
ctccttaagt gcacacaacc tcagctgacc acataggtgg cagtgatagc aaatggtgag
                                                                      960
gtgggtgggg gtgggggtcc tgcagctcac tttctgtnct gcgtaataag ggagagatca
                                                                     1020
gagatgcata gacttttaaa ctggtacggt tcttagagat ggtccttggc cttctgttgt
                                                                     1080
1140
cttctttttt ttttcagagt cttgctctgt caccaagact ggagtgaagt gatgtgatct
                                                                     1200
cggcttactg caacctccac ctcctgaggt caggagaatt gcttgagagg cagaggttgt
                                                                     1260
tgtaagccga gatcgcgcca ttgcacgcca gcctgggcaa caagattgaa actcccatct
                                                                     1320
caaaaaaaa aaaaaaaac tcgtag
                                                                     1346
<210> 42
<211> 998
<212> DNA
<213> Homo sapiens
<400> 42
```

```
ggtgtcctgc ccgtttttgt ccttaatggc cgtgttgatt cgataggaat cgacagatgg
                                                                          60
 gagccaagag gggacgtaac cacttgccag tgtggcccag tatttatatg gtagaagctc
                                                                         120
 gggctggcat tgagatggag gtgggaaaga ggagggtgtc tcgtgtttaa agatttctct
                                                                         180
 cttgtgtggt ccttggttat ggctccccat ggtgcttgct gctcccttgg tcgcctttcc
                                                                         240
 ttgcattttg ctttttgcct ttagtccttc tgcagtcagg gaccatgttg gtgactctcg
                                                                         300
 gtcagatgtt cccatatttg catgtcttgc tttggcctct ctggctctag gttctgtatt
                                                                         360
 gctagttgct ttctgacatt ttttctcatt gtttgtgcta ccttggccaa gaacctcttt
                                                                         420
 geetteteee tegttigtaa eatigagate etagtageag tiaettetta gggtigtiag
                                                                         480
 gatgacatga gatgggcgag ttggccatct gccacacaag agttcccttc tcactgccat
                                                                         540
 cctctgccca gggtgttccc cagaatctgc agggccccat tggtcatctt gctgtctgca
                                                                         600
 caccttcctc tctcacctct tggcacttcc ctcaaaaaag agagaagtgg agcacagtaa
                                                                         660
 ataaacgcca gcgttttctc cagttcccag cacctctccg gaactggatc ccccaaactc
                                                                         720
 ctctgtcact ttctgtgtcc agcgggcccc tggggtcctt cactgtcttc actctgctca
                                                                         780
 gcctgtgcgc ttggccttgg tgctgtaggg actgttataa gagctgctgt ccgatcccca
                                                                         840
 tattcaatct cacageeeca etttgtgtae acacaceaga geeatettet taaaateaga
                                                                         900
 tectgteact ecteteceta aaatetacea gtggtetaat aaaatettga atttttagea
                                                                         960
 taaaaaaaaa aaaaaaaaa aaactcga
                                                                         998
 <210> 43
 <211> 658
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (6)
 <223> n equals a,t,g, or c
<220>
<221> SITE
<222> (15)
<223> n equals a,t,g, or c
<400> 43
acgacnagac aggtnaccgg taccggaatt acccgggtac gaacccacgc gtaccgatat
                                                                         60
ttcgtcattt aagaatatct acagatatgc ctttgatttt gcaagggata aagatcagag
                                                                        120
aagccttgat attgatactg ctaaatctat gttagctctt ctgcttggga ggacatggcc
                                                                        180
actgttttca gtattttacc agtacctgga gcaatcaaag tatcgtgtta tgaacaaaga
                                                                        240
tcaatggtac aatgtattag aattcagcag aacagtccat gctgatctta gtaactatga
                                                                        300
tgaagatggt gcttggcctg ttcttcttga tgaatttgtt gagtggcaaa aagtccgtca
                                                                        360
gacatcatag caagaactat gtgaagaaaa tgcaaacctt tcaattccca cgtgtataca
                                                                        420
agctaatgtg atgaggggga aaaaaatcca acgggtgcat tttcattcat atgaaagact
                                                                        480
totcatagta ctttttttc cttttttaa aggaggtttt tcttgttaca tgtgatgggc
                                                                        540
attgagccac acctettett agactgaata ttgaagtttt tgttttgagt tatgtttata
                                                                        600
acatttattt cagaacaata aagattcaga tttgtgacaa aaaaaaaaa aaaaaaaa
                                                                        658
<210> 44
<211> 566
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (68)
<223> n equals a,t,g, or c
```

```
<400> 44
ggctatttag gtgccctata gggaaagctg gtacgcctgc aggtmccggt ccggaattcc
                                                                         60
cgggtcgncc cacgcgtccg gtcagagaga aagaactgac tgaaacgttt gagatgaaga
                                                                        120
aagttctcct cctgatcaca gccatcttgg cagtggctgt tggtttccca gtctctcaag
                                                                        180
accaggaacg agaaaaaaga agtatcagtg acagcgatga attagcttca gggttttttg
                                                                        240
tgttccctta cccatatcca tttcgcccac ttccaccaat tccatttcca agatttccat
                                                                        300
ggtttagacg taattttcct attccaatac ctgaatctgc ccctacaact ccccttccta
                                                                        360
gcgaaaagta aacaagaagg aaaagtcacg ataaacctgg tcacctgaaa ttgaaattga
                                                                        420
gccacttcct tgaagaatca aaattcctgt taataaaaga aaaacaaatg taattgaaat
                                                                        480
agcacacage attetetagt caatatettt agtgatette tttaataaac atgaaagcaa
                                                                        540
aaaaaaaaa aaaaaagggs ggccgc
                                                                        566
<210> 45
<211> 1277
<212> DNA
<213> Homo sapiens
<400> 45
ggcacgagga ataatcctag ctctatctgc agggttttat cgtggtttcc ctgagtttaa
                                                                         60
acatgtaaca ggggagcaga aggagggata aatgatttgt ttatgctcaa taaagatgtt
                                                                        120
getgetgtte tgteagetaa cetttgetet cataacetge ataaacetge aaagtettta
                                                                        180
tttattctcc taccagcaaa ttattggaat tcatagtcat gtctaatttt agttagctta
                                                                        240
gggatggcac tcaacagggt tataaaaggg ggagaacatc tctctcattc ctgaatttcc
                                                                        300
aaggctggga ttacggtaaa gctgtgggag atcacagtaa ttgaggtttc ccaggacact
                                                                        360
cccatagtgg gttatgcttc ccaaatctgg ctttctaagc ataatggaat ctggcctaac
                                                                        420
ctgtcttcca atatttgagt ctcttctata gcacccctgt cagagtggtt tgtgttcttc
                                                                        480
acttgataaa aacttttttg gggatgcatc attacagttt gagccaggtg atttcatctt
                                                                        540
caggcagctg tgatagataa taatacacaa taaggaaaca acgaaacact ttttaatgga
                                                                        600
ttagtaagtg ggaatagata gggcacctgt catttcattg ttgtccgcat gacctgatga
                                                                        660
ggtagttaac tgttagtgtc acttccattt tcaggccaaa aactgggggc ttggaatagt
                                                                        720
ggagcaactc cggcagtgcc acacagctat gaaatatcag gtcagaaccc cagggatact
                                                                        780
ggatccaaaa acctgagagg aagctatata tcctttaact tcttcaccca aagctgaaat
                                                                        840
ctgcttccta gttctatcct ccaatgaccc aaggaaaaga atctcttccg ctacttgctc
                                                                       900
ttcagatatt taacacaact ttcaggcctt cttttgcatt cttttcaggc cacaggacac
                                                                       960
tgtttttcgg tgttcgttcc cccaaccccc ccaaaccacg tatttttctc atttggctta
                                                                      1020
ttgcagtagc tctctaaagg tctgcctgct ctgttcccta ttcttcaccc agcagccaag
                                                                      1080
gccacgctta aaatacaagt caaatcactt cattcctctg ctcagaacac ttctgcagtt
                                                                      1140
tttcctgtca cttgaggtaa aaccttaagt caacttgaag attacagaat tgaattgtct
                                                                      1200
tactgaaatt acctttccaa aatcgatggt tcccaactcg tgccgaattc gatatcaagc
                                                                      1260
ttatcgatac cgtcgac
                                                                      1277
<210> 46
<211> 442
<212> DNA
<213> Homo sapiens
<400> 46
gaattcggca cgagggctga gtgggggcca tccttttcca tggctgagtg agggccatcc
                                                                        60
tttcatgtgg ctgagaggga tccatccttt cctgtggctg agcgggatcc attctttccc
                                                                       120
gtggctgagt ggaggcccat ccttaggtac ctccagtgag cagcctacat ccttggagga
                                                                       180
tggaaaattg atttgcctct tcacagactt ctctggttct agctttgggc tatttatgcg
                                                                       240
tgaagctgct aagaacattt cccaaatgtg atttgtataa atacctagga gtaggattcc
                                                                       300
tagtgtgagg tcagagtctg tctagcagca taaaaacaac caaaagattt tctgagcctc
                                                                       360
agggcacatg ggtggggccc agagagcacc caggaccgaa gctgcccagg acctccctcg
                                                                       420
```

```
aggggggccc gtaacccatt cg
                                                                            442
  <210> 47
  <211> 890
  <212> DNA
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (818)
  <223> n equals a,t,g, or c
  <220>
  <221> SITE
  <222> (819)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (829)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (859)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (887)
 <223> n equals a,t,g, or c
 <400> 47
cttgtaaatg tttcttttcc cttaaataca gataattcat ttgtattgct tattttatta
tgagctacaa caaaaggact tcaggaacaa gtaatgtatt agtatggttc aagattgttg
                                                                           60
ataggaactg totoaaaagg atggtggtta ttttaaatat aaatagotaa tgggggtggt
                                                                          120
aggeetataa aattaaatge ettgtataaa ateeaaaatg aatgeaaaat tgtttteaet
                                                                          180
tgtattgact ttatgttgta tgattccaat ctctgttctg tttggcactt gtatttaatt
                                                                          240
cttcaccttt gtaagacatt tgtatattgt ggatgtgttc attcaagcta tttaatatct
                                                                         300
ggcactgtta atacacagta ctttattgta cagactgttt tactgtttta attgtagttc
                                                                         360
tgtgtacttt ttttggatgg ggctggcatg ttttctttgt ttcctggcaa tacgacgtgg
                                                                         420
gaatttcaat gcgttttgtt gtagatgcta acgtgtcaga atcctttaca ttcaactttt
                                                                         480
ctaagaaaag cattttcagt cttgtagtgt gtgcttacag taactaattt tgttgaaaat
                                                                         540
ggtttcaagt tattcaaatt tgtacaggac tgtaaagatt tgttgacagc aaaatgttga
                                                                         600
agaaaaaagc ttatagaata aaagctataa agtatatatt aggatctgca aacaatgaag
                                                                         660
aattatgtaa tatattgtac aaatgtaagc aaaggctctg aaataaaatg ccatagtttg
                                                                         720
tgaaaaaaaa aaaaaaaaa actcgagggg gggcccgnna cccaatcgnc caaaagtgag
                                                                         780
togtattaca attcactgng cogtogttta caacgtogtg actgggnaaa
                                                                         840
                                                                         890
<210> 48
<211> 737
<212> DNA
<213> Homo sapiens
<220>
```

```
<221> SITE
  <222> (736)
  <223> n equals a,t,g, or c
  <400> 48
 gctgcgagaa gacgacagaa gggggagctc accagcgcca ccgtccccgg cgaagttctg
                                                                           60
 cgctggtcgg cggagtagca agtggccatg gggagcctca gcggtctgcg cctggcagca
                                                                          120
 ggaagctgtt ttaggttatg tgaaagagat gtttcctcat ctctaaggct taccagaagc
                                                                          180
 tctgatttga agagaataaa tggattttgc acaaaaccac aggaaagtcc cggagctcca
                                                                          240
 tcccgcactt acaacagagt gcctttacac aaacctacgg attggcagaa aaagatcctc
                                                                          300
 atatggtcag gtcgcttcaa aaaggaagat gaaatcccag agactgtctc gttggagatg
                                                                         360
 cttgatgctg caaagaacaa gatgcgagtg aagatcagct atctaatgat tgccctgacg
                                                                         420
 gtggtaggat gcatcttcat ggttattgag ggcaagaagg ctgcccaaag acacgagact
                                                                         480
 ttaacaagct tgaacttaga aaagaaagct cgtctgaaag aggaagcagc tatgaaggcc
                                                                         540
 aaaacagagt agcagaggta tccgtgttgg ctggattttg aaaatccagg aattatgtta
                                                                         600
 taacgtgcct gtattaaaaa ggatgtggta tgaggatcca tttcataaag tatgatttgc
                                                                         660
 ccaaacctgt accatttccg tatttctgct gtagaagtag aaataaattt tcttaaataa
                                                                         720
 aaaaaaaaa aaaaanc
                                                                         737
 <210> 49
 <211> 571
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (249)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (548)
 <223> n equals a,t,g, or c
 <400> 49
tcgacccacg cgtccggggg cgtacgcggg caagatggag gcgactacgg ctggtgtggg
                                                                         60
ccggctagag gaagaggcgt tgcggcgaaa ggaacggctg aaggccctac gggagaaaac
                                                                        120
cgggcgcaag gtgagaagtg tggagtgagg gtcgcagttg aggcgtccag cgttcggggt
                                                                        180
ccgggtcgcg cttgaggaga gcaaagggct aataaggaaa gacagctgcc gagggcgcgc
                                                                        240
atgccgggnc gctaacgcat gcgcgagaag acgggcgccc tcccacgatg tctggggctg
                                                                        300
cttggcgtgg gactcctctg gcgctggtgc ggtcgtcgcg cacgcgcggg ggtgggcaar
                                                                        360
gcatggtcag cgacccgcag tccatctgac tcctgcttcc cgggtgttgc tcgtgtaggt
                                                                        420
atctagggct gcctgtaggt tcagatgctt gttgggttag gcgtgatttg ttccgttcct
                                                                        480
ctatggccta gctggtcttt aacccccgcc ttcgattctg agtcagacag actccccagt
                                                                        540
tcgggcangc aattcccttg gaacaagggc a
                                                                        571
<210> 50
<211> 356
<212> DNA
<213> Homo sapiens
<400> 50
ccacgcgtcc gtaaaactcc acatttgtct gcatcaggga aaatgcatgg gcacacatcc
                                                                         60
tecetecete ectetetaet etectecett ectteaggee tettageatt gtttgtttte
                                                                        120
ccatttctga tactactact ccatgctgaa gatttgccat attactattt tggaaacatt
                                                                        180
```

```
gagtgataga actcctagaa aatttgcaaa gaaatgttac atactgtata tcaaactctc
  agattctagt gttgaaaaag tagcctatac tttgctatta cttatacctg ctgccataga
                                                                        240
  aaaaaaataa gtttattcat gacacattta catttgatca taaaaaaaaa aaaaaa
                                                                        300
                                                                        356
  <210> 51
  <211> 913
  <212> DNA
 <213> Homo sapiens
 <400> 51
 ggcacgagtt agtgtcctga aacgcctatg acagtgcctg gcccagggtt gggcacttac
                                                                         60
 tcatgttatt cacttattca tatgtgggaa tgaacagttc agccagtata aaggacaggt
 gagtacacac caaggagatc ttcagggaga gatcagctgg ttttcctgtg aagatgtcag
                                                                        120
 cttcatccct ccaccgtctc cctgtgctca tggctctgtt ccctttccag gctgctgctg
                                                                        180
 ctggttcttt gggtctgcag ccacctccca cccccatgaa gggcaaaccc agcartatgt
                                                                        240
                                                                        300
 ttgctcttgt cagctttggg agggcagact ccatagttgg agatgggctt ccaaccaacc
                                                                        360
 aaggagataa atgccagagg gagcgaacca tgccaggctc aaagcacatc tctccccaaa
                                                                        420
 ctccccaggt ggggaagcag gccagaggct ccacaaaccc ctcagggagg cctggagtcc
                                                                        480
 agatgctgta ctccagtatc taaacaatca ctgaatctta aagctgacag gttcaaagct
                                                                       540
 cttactttgg gccgagcgca gtggcttacg cctgtaatcc aggcactttc ggagctgagg
                                                                       600
 tgggtggatc acctgaggtc aggagtttga gaccaaccta gccaacatgg tgaaaaccca
                                                                       660
 tototactaa aaatacaaaa attagotggg ogtgttgaca ogtgootgta atcocagota
                                                                       720
 ctcggtaggc tgaggcagaa gaatcgcttg aacccaggag gcagaggttg cagtgagctg
                                                                       780
 agatcatgcc actgcactcc agcgtgggtg acagagtgag actcccgtct tgggaaaaaa
                                                                       840
                                                                       900
 aaaaaaaaa aaa
                                                                       913
 <210> 52
 <211> 1356
 <212> DNA
 <213> Homo sapiens
<220>
<221> SITE
<222> (1231)
<223> n equals a,t,g, or c
<400> 52
cccacgcgtc cgaaagaatg ttgtggctgc tcttttttct ggtgactgcc attcatgctg
aactctgtca accaggtgca gaaaatgctt ttaaagtgag acttagtatc agaacagctc
                                                                       60
tgggagataa agcatatgcc tgggatacca atgaagaata cctcttcaaa gcgatggtag
                                                                      120
ctttctccat gagaaaagtt cccaacagag aagcaacaga aatttcccat gtcctacttt
                                                                      180
gcaatgtaac ccagaggtat cattctggtt tgtggttaca gacccttcaa aaaatcacac
                                                                      240
ccttcctgct gttgaggtgc aatcagccat aagaatgaac aagaaccgga tcaacaatgc
                                                                      300
cttctttcta aatgaccaaa ctctggaatt tttaaaaatc ccttccacac ttgcaccacc
                                                                      360
catggaccca tctgtgccca tctggattat tatatttggt gtgatatttt gcatcatcat
                                                                      420
agttgcaatt gcactactga ttttatcagg gatctggcaa cgtagaagaa agaacaaaga
                                                                      480
accatctgaa gtggatgacg ctgaagataa gtgtgaaaac atgatcacaa ttgaaaatgg
                                                                      540
catcccctct gatcccctgg acatgaaggg agggcatatt aatgatgcct tcatgacaga
                                                                      600
ggatgagagg ctcacccctc tctgaagggc tgttgttctg cttcctcaag aaattaaaca
                                                                      660
tttgtttctg tgtgactgct gagcatcctg aaataccaag agcagatcat atattttgtt
                                                                      720
tcaccattct tcttttgtaa taaattttga atgtgcttga aagtgaaaag caatcaatta
                                                                      780
tacccaccaa caccactgaa atcataagct attcacgact caaaatattc taaaatattt
                                                                      840
ttctgacagt atagtgtata aatgtggtca tgtggtattt gtagttattg atttaagcat
                                                                      900
ttttagaaat aagatcaggc atatgtatat attttcacac ttcaaagacc taaggaaaaa
                                                                      960
                                                                    1020
```

taaattttcc agtggaggat a tttgacgatc acttatatca c ttgtaaatgg atggataaaa ttcacaccaac agttgattat a tgttgaccat ttctacaatt tcatccaaaaa aaaaaaaaaa	ctegtatat gactaagtaa tggaattac teatatacag stattteetg natateagee gtaaaaagte caatetgtge	acaaaagtga (ggtgggattt (cctaatagga (gaagtaatta tatcctgtta	1080 1140 1200 1260 1320 1356
<212> DNA <213> Homo sapiens				
<400> 53				
ggcacgagcg gctgcgggcg c	gaggtgagg ggcgcgaggt	teccamana	.	
tctgcaggaa gctgaagtga g	aggcccaga gacgcgaggc	ccccagcagg a	rgccccggc	60
caaggcccgg ctgttccggc tg	ataactaat actaaactaa	ceegeeeggg g	caggatgac	120
catcgtgtac tgggacagcg ca	agcaccaca cacttotact	tanananata -	cctgctgat	180
ccgcacacgg ggccgccgct gg	managed caccadaca	rgcacacgee c	ttctctagg	240
actecgatgt egaegagttt ei	Eggacaatt totoatooto	ggacagggag c	tcacggccg	300
cccagaaagg agacggagca go	Cacctaca ccaaaaaaa	gegegaagea g	agtgacctt	360
ctacgactgg tcccggggg ac	Cacceaged cedddddage	atggaggaga g	cgtgagagg	420
ctacgactgg teceegegeg ac	cttctgggg cageceagae	cagggccggc a	gcaggcgga	480
gcgcaggaac gtgctgcggg gc	Caactogge Caactocage	ctggccttcc c	caccaagga	540
gcgcgcattc gacgacatcc co	accessage access	ctgatcgtgg a	cgaccggca	600
cggggccatc tactgctacg to	Teaceasa tagasata	aactggaagc g	cgtgatgat	660
cgtgctgagc ggaagcctgc tg	Sacces sates	egegaceege to	gcgcatccc	720
gcgcgagcac gtgcacaacg co	Catalagat catalagae	aacaagttct g	gcgccgcta	780
cgggaagete tecegeeace te	Schaptata caagetcaag	aagtacacca ag	gttcctctt	840
cgtgcgcgac cccttcgtgc gc	cocatas states	agcaagttcg ag	gctggagaa	900
cgaggagttc taccgcaagt to	racettan	gtgtacgcca ac	cacaccag	960
catcagtac ctgctggacg ag	gettteeg egetggeete	aaggtgtcct to	gccaactt 1	.020
catccagtac ctgctggacc cg	cacacgga gaagctggcg	cccttcaacg ag	gcactggcg 1	080
gcaggtgtac cgcctctgcc ac	cegrgeea gategactae	gattcctggg ga	agctggag 1	140
actotygacy aggacyccyc yc	agetgetg cagetactec	aggtggaccg go	agtccgct 1	.200
tecceegag etaceggaac ag	gaccgcca gcagctggga	ggaggactgg tt	cgccaaga 1	260
tcccctggc ctggaggcag ca	gctgtata aactctacga	ggccgacttt gt	tctcttcg . 1	320
gctaccccaa gcccgaaaac ct	.cctccgag actgaaagct	ttcgcgttgc tt	tttctcgc 1	380
gtgcctggaa cctgacgcac gc	gcactcca gttttttat q	gacctacgat tt	tgcaatct 1	440
gggcttcttg ttcactccac tg	CCtCtatc cattgagtac	tgtatcgata tt	gtttttta 1	500
agattaatat atttcaggta tt	taatacga aaaaaaaaaa a	aaaaaa	1	547
<210> 54				
<211> 1338				
<212> DNA				
<213> Homo sapiens				
<400> 54				•
cccacgcgtc cggttccccc atc	ctgtctct caggagcgag a	itctgatcgc tg:	2255500	60
	gctgcttg catatettta c	atogcacco co:	20200220	60
addiced and concept aga	atgactca gtccgtgtgt a	taatgccag cad	TC2CC2t2	120
getter Lyaagcaccg got	tgcagoga aatgtggcgt c	tetageeta as	.~~~~	180
-sedected terragetat ago	cctgccag agctgcattc t	tatctggac oct		240
	cttctggc tqtqcccaaq t	actatetes cod	tagaast :	300
and occurred coagonings of	gggccccc agtggggggc g	OCCOCCCC and	sttenese /	360
-sawegerge tateegggta tgg	gatgici caacagagac c	tatatecee et		120
ttcgaggagg tggggtgacc aac	tgetetg gteeceagae g		tecetggt 4	180
	2 2 2 2 2 2 2 2 3 4 C 9	J-my-addd (CC	Lygctac 5	40

WO 99/31117 PCT/US98/27059 27

cactccttca	gctgtctttc	gagtctggga	ggcccagatg	tggacttgtg	agaggtggcc	600
	gggcgctgtc	agactggctg	ctggagccca	gatggcagcc	gactgctgtt	
cactgtattg	ggagagccac	tgatttactc	cctatctttt	Ccagaacgtt	ataataaaaa	660
aaaggggtgc	gttggaggtg	caaagtcagc	aacgatrata	acadatetat	gragegaggg	720
aatacagaca	ccagatggtg	aggagagget	taaaaaaaa	gatastas	Ctyagacaac	780
cccagtaga	gaacgtetgg	Ctataattat	cgggggagag	gereaereea	tggtctggga	840
accartests	gaacgtctgg	cigigettat	gaaaggaaag	ccaagggtac	aggatggtaa	900
actugecate	ctccttttc	gcactcgaaa	cagccctgtg	tttgagctcc	ttccctgtgg	960
caccaccag	ggggagecag	gagcccagcc	ccagctcatc	actttccatc	ttccttcaac	1020
aaaggggccc	cyclcagtgt	gggctggtcc	acaggccgaa	ttgcccacat	CCCGCtctct	
tttgtcaatg	cccagtttcc	acgttttagc	ccagtactta	aacaaacccs	aganasas	1080
gctgggggtg	gaggetetat	tcatgacctg	coostatit-	ggcgggccca	ggaaccccct	1140
gcccttaga	gaggetetat	2000000000	CCCCCCCCCC	ctgagacatc	cccaacctct	1200
ctctaacaat	accetetece	agggccacca	cctgttctgc	cccactcccc	acattcccac	1260
	aaataagttt	tccttttgtt	ttccaaaaaa	aaaaaaaaa	aaaaaaaaa	1320
aaaaaaaaa	aaaaaaa					
						1338

<210> 55 <211> 2071

<212> DNA

<213> Homo sapiens

<400> 55

cggcacgagc caaaacaaaa attttgtgca gtcctgtcat ttaatcatct tatcagtgcc ccaaggtgac ttttttcaag agctctgttg ataccatgtg tgtgtgttat tttctggtgt 60 ttttacagat ttgggccagg cttagtcatc tattggtatg gatttatcca ggagctggac 120 tgcaaccggg aaaggggcat cctgctcaaa gcctgtttcc ccacgaacat tgtcacctta 180 tgccacagca tagcttgacc ctgaagatcc tggaagagaa gctgggagga aaaggtgaat 240 ccggaagcaa ttttactttc ctgcactgta agatcctggc aacatctgcc ctgaacttca 300 getgaactet tgetgeeegt agteacacca etacetettt agacaaacat atcaagagtt 360 420 tctgttttcc ttcatccctt gctgatgtga acagccaaga actacagaca caacccactc 480 attatcagca tttctgtctc tgtcaaacaa ttagtttata gatagtcata atctttcttt 540 cttccggatg gtttatcctt gtatgctgaa caaaagaaaa aatgtgaaga ctgaaaggtg 600 tgatttttca attctcctcc cagttaccga atcaccctcc ttatttttt ttccctaagc 660 ctccgttcac tgtctctccc tctccctttc tctttccatg ttgcactcca cagagaaccc 720 agcattgcat taccatcgtg gaataatcta gcgcaaacct aggaaagctg aagccacaaa 780 gtccaaagcc acctttgtac tcacctgcag agctccagaa gaccttgatg gcagcctgcc 840 tatgctgtgt gtttgctata ttcaatcttt acggcttcct gacttctgtg acagtaagcc 900 aagtgcaaaa atacacttga tgagaatttc ctcttttaat aatgttattt gaacaccaca tattttagat ttatcttatt tgaaagtatt agttccattg tgcctggaaa ccacactcct 960 1020 ttagattggg ggccgagagg cgacaaccca acattgagga gagtttattt ttaaacatgg 1080 ctagttgtca gtatgtacgt gagctagtat ttttatgagt cgagtttttt aaaggcacat tctgtatact gcttagtata tgcattttat accatgtaat tataaaacac tcgagtaagt 1140 tcagcattag aaatgtttag ctttgtatga actgagtgtg ccagaaataa acctggagca 1200 atttttaaat aagcaaaata aaggagattt ttctatttgt tcactttaat ttattcactt 1260 ttgtgtactt ttatgtactg caaatcagat ttcagtctaa agcgaaacat caataagtta 1320 ataataaacc tatettttgg gaagttgaat attaatetgt acccaaaacg tatttagtaa 1380 aatatttgcc cccgccaccc tgccatgctg acataacaac ttttataatg ttgaatagat 1440 gatatgggaa atactaataa caacaatgta atttttgcag acagctttaa cttatataca 1500 ttggttgatt tttttcaaaa gactaaatat gtcatttata ctttgtttat tttctaccaa 1560 agaaggtttg taaaaatatg cctgctgctt ttccttttga aggacacaaa cctggtccca 1620 acatgtgtgg attttaactc tgagtggggt gcattaaatc aaaagagaga ggcagaagat 1680 gaaatgctaa agaagggtca ggcaaacttc tgtttcagta taaaattcat catgcaggct 1740 totgagtgaa atagaatgat ttgaaaccac tactgtattg cotggataca cacacacac 1800 cacacacaca cacactttat acaaaaatgt taaaagcagg tttcctggca tgttctaaac 1860 tgtttttttt ttaggaataa attacattta tctgcacaga tgttgaaaat cctgttaaac 1920 ccttgtcaag gatttgttta ttttacatta aacaaattta ttatgatgaa cgtgaacaaa 1980 2040 taaattaaaa aaaaaaaaaa a

```
<210> 56
 <211> 1899
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (1439)
 <223> n equals a,t,g, or c
 <400> 56
 ccacgcgtcc gcccacgcgt ccgcccacgc gtccgttacg atttataaaa gcaaactttt
                                                                          60
 aatttttcat aatatatcta ttcctaccta ggttttttta atcaaattaa taaaatggta
                                                                         120
 ctcccttttg tgttattgtt cagaccaaat tttatcagtg tccttcaccc tttattctac
                                                                         180
 tcacattgtt tatttctata cttaataagt cctgttcact cttcctctat aatatattac
                                                                         240
 aaacctgatc attgtcacta caccccattc attcctggtc tactacaata gccaggtcta
                                                                         300
 cctactttcc tttcggcatt tggacaatct gtgtttctgg aagtagccca aatgatcttt
                                                                         360
 ttttgttctt atattattca gatcctatta ctccttgatc tcaaccccta caagatattc
                                                                         420
 ctattatatg cttaataaaa tccaatatcc ctaccttggc ctgtatactc aataaagtcc
                                                                         480
 aatatcccta ccttggccta caagatctta gatgactggg atctaggaaa cctattcagc
                                                                         540
 taatttcctg caattctcta tgtttacctg ctcaaggttt ttaccactcc tcaaatattc
                                                                         600
 aaactggttt tgcatctttt tagttctatc tattcttttg cagatgccaa tcttagtaat
                                                                         660
cataagcagt ttacctctaa attaatgcta aatattgtaa aaggtgtatt ataagttcag
                                                                         720
 tettteattt attettteaa ceaccaagtg tegattgaac acatacattg ggteacacea
                                                                         780
atcaaataag atagactccc aggcatcacc gagcatctac tactcaattc atctcaggat
                                                                         840
ctatacaagg ggtcatttta tcagaaacca aagtcttgat gctgtccgaa aaatcacgtt
                                                                         900
ttcaccatga tctcctactt ccctaggtgg aagtataact ttttaggata tatcatggtt
                                                                         960
gctgacttaa cttttgtatt ttttaaatat actcatgaca agtatcatat aaaacctaac
                                                                       1020
cagcaacttt gcaccagcaa aagtttttca acatttcaat tcttacaaaa tcaaatgata
                                                                       1080
taattteeta tgtagtaaaa aatteacaca tetgeaaage ttggttteae taccacetgt
                                                                       1140
taaaatctta cctttggaag ctatttatga ttgaaaaaca ctttacctca ctcacaaaga
                                                                       1200
gctggaagtc tctcttcaat ccaatatgca cacagaagac aaaaagctgt atcattcctt
                                                                       1260
gatgatatat ttgaaatcat atggccacgt ctgtccattg tcttcagagt ttctaagtat
                                                                       1320
ttcagaaaat tatgacttgc actgtagaac tattttaaag aaattccatg gtgcaaacag
                                                                       1380
aaaaactaaa acttttcatg ttaggataat ttattaaaaa tacaaacaaa tcctatgtnt
                                                                       1440
acataagaag atagtaacta gcctttttga gagggaaatt tttctctcat aacttctttt
                                                                       1500
ctagtaattt caataaagaa taactgccat tccaacgttt agcccatctc actctttgt
                                                                       1560
cttcttatgg ccaagtattc aagcttgaaa tttgcagagg aaattcttgt ccgtttttta
                                                                       1620
tatcatgtgg taagcctaat aaaacatctt ctgaaataat tagcccttaa aaggatagta
                                                                       1680
tcttctacct gacagaggca aatattattg aaaagtttgt accttataag cacattaatc
                                                                       1740
atggagteet ggaactggat tetgtetaag actgaetttt gettaattaa gtteacagag
                                                                       1800
attttccaca tatttttcca gaacattgca tgtagagata ttgtcgatca atcacataac
                                                                       1860
tagggtcaga aagatgtaac aagggagaaa aaaaaaaaa
                                                                       1899
<210> 57
<211> 1543
<212> DNA
<213> Homo sapiens
<400> 57
ggcacgagat ttgattctca tgctcctttc aaaagagcat actagtttgg ggtggttggt
                                                                        60
tattttctta accttagcaa gccagcttat ttcctatgga agcagaactg gaaacagcag
                                                                       120
atgtccacca tgcttataca ggacactaca cactgtctcg acaagccatg ttctttcctc
                                                                       180
cctcttcgtg agcactttct ctggtgatga gttagtatgg actacttgaa cctcaaaact
                                                                       240
```

```
gggcctctca cccaaagcca aatgaagtag cgtatgccag gatgatgttt cttttgggcc
                                                                       300
  gttggcagtg agactgctaa gcaggctgcc ttaggttttg ctgtggcaat gctagcagat
                                                                       360
  tgttccctct ttcaaagggg caaaaatatc attttggtat gataactgac tttctattta
  cagtttctgg cccccaaaga caaaccaagt ggagacacag cagctgtatt tgaagaaggt
                                                                       420
                                                                       480
  ggtgatgtgg acgatttagt aagtactttt aatatgcacc tggtgttctg tgattgaagt
                                                                       540
  cacctgaget gtaaatacag ccacaaagge tgattatett acacttgttg ettatttgtg
                                                                       600
  ttttaatttc caatacacca gaagcttcct acaccattat atattgccat tataaattca
 atcagatagg taatttcata atagaaattc ctgtgtttca tggtgtcggc tatattgttc
                                                                       660
                                                                       720
 attcagatta atcctctccc ttgaagggct gaaaaagact agggagctat tccattagta
 gcaaaatgtt gtaattcact gaaattgctg ttaaccaaaa ataagtaata caacatggca
                                                                       780
                                                                       840
 ttttgtgtgg gttgacaaat gaaacaggcc ttaaaagggc tacttcttaa atgttctcaa
                                                                      900
 ttaacttaat gtaaacaaaa tagaccgata ggcatttgag gatttctgga ccccattaca
 ccatgttgtt gatgtctggg aagctgtgta gtaaatgtct tttgtatcta tccttaatgt
                                                                      960
                                                                     1020
 ttggaaactt cccgccttta agcttcatat gacaactgac caacaaacac tacgtactat
 gatgtcaatc ttttttagag acattctcat tactaaaatg agtggatact tgaatgttta
                                                                     1080
 actcctaaaa taatgagcgg tgaataaatg agcaagtaca tgcatgcctt ccaatgtaga
                                                                     1140
 gtcattttca ttaaaccctc tctcaccaga gaagcagtgg tatgaaattg gcctgattcc
                                                                     1200
 tttctaagtg tgttgttctt gttcacagtt ggacatgata taggtcgtgg atgtatgggg
                                                                     1260
 1320
 gccattcaag gggagccaaa atctcaagaa attcccagca ggttacctgg aggcggatca
                                                                     1380
                                                                     1440
 tctaattctc tgtggaatga atacacacat atatattaca agggataatt tagaccccat
 1500
                                                                     1543
 <210> 58
 <211> 1133
 <212> DNA
 <213> Homo sapiens
 <400> 58
ggcacgagct ggagcaaaga tattgtttga aggagagttt atggttttgg attttaaacg
ggcagggtct tttttcctct catttttgtg gacaagagag gccttcgcct ttattttac
                                                                      60
                                                                     120
tctccctctt ctgctgtccc tgtgcagagg aaaaatgaag aattctccca gaagtgactt
gtcaagactt aaaaaaatg tttttaatgc átttcttcct tgtctagtgc ctcggtttat
                                                                     180
ctctaacagg ggctgtccag tatatcggtc ctgttaggag gggagaaaaa gttcttccaa
                                                                     240
aggctggaga agtgaacaag gagtcaaatt tattttccca attcaacttc ataattatca
                                                                     300
tttctttggc ttcatgctct cccgtaactc atgtggttgg gatccatccc atctgggtca
                                                                     360
cttcagtcta cttcacytac ttgaaaaggc tttcctttac acttccagga ccaaacagca
                                                                     420
                                                                     480
acttcctgcc acacacttcc accctatcac tgggagaaat ccttttctgg acatgagcct
                                                                     540
ttgacctggg tggggcagaa agaaccacaa actccatctc ccaatagaac tttgaaattc
                                                                     600
actcagcttt tcctttcatg ctgtttgttg cctgcttgtt gcactcctcc tgccccagaa
                                                                     660
ctgcaagatt tttagcttca cccctttctg agagtaatgt tatctttat cagaatcagt
                                                                     720
atcagttccc ctgtattctg tgcttcatcg aatttgcaag actgacctct tttaagcatt
taattcactc ccagagtcat ctggtcaggt tgcaatatga ggacttctct gtctcctctg
                                                                     780
aagcctggga cactgagctt acttaataca ttagatgttc aaaagaggag cgttgtttca
                                                                     840
                                                                     900
totttcaaaa tgttaggcca ttactttgag tataaaatcg acttattaat gattagtaat
ttttctaaag tattgggaaa actttcttat tttataagat cttaacaagc ttaaaaaaga
                                                                     960
                                                                    1020
attttatgac cagaatccaa caagagctct attttggaat tgtgcccaag ttggtgatgt
ttactctaaa attaataata aaactacttg taagcaaaaa aaaaaaaaa aaa
                                                                   1080
                                                                   1133
```

<210> 59

<211> 1490

<212> DNA

<213> Homo sapiens

<400> 59

```
ggcagaagtt cctctgcgcg tccgacggcg acatgggcgt ccccacggcc ccggaggccg
                                                                       60
gcagctggcg ctggggatcc ctgctcttcg ctctcttcct ggctgcgtcc ctagacatca
                                                                      120
eggetgeage cetggetaeg ggtgeetgea tegtagaate etetgeetee eceteateet
                                                                      180
gctcctggtc tacaagcaaa ggcaggcagc ctccaaccgc cgtgcccagg agctggtgcg
                                                                      240
gatggacagc aacattcaag ggattgaaaa ccccggcttt gaagcctcac cacctgccca
                                                                      300
ggggataccc gaggccaaag tcaggcaccc cctgtcctat gtggcccagc ggcagccttc
                                                                      360
tgagtctggg cggcatctgc tttcggagcc cagcaccccc ctgtctcctc caggccccgg
                                                                      420
agacytcttc ttcccatccc tggaccctgt ccctgactct ccaaactttg aggtcatcta
                                                                      480
kcccwkctgg gggacagtgg gctgttgtgg ctgggtctgg ggcaggtgca tttgagccag
                                                                      540
ggctggctct gtgagtggcc teettggect eggeeetggt teeeteecte etgetetggg
                                                                      600
ctcagatact gtgacatccc agaagcccag cccctcaacc cctctggatg ctacatgggg
                                                                      660
atgctggacg gctcagcccc tgttccaagg attttggggt gctgagattc tcccctagag
                                                                     720
acctgaaatt caccagctac agatgccaaa tgacttacat cttaagaagt ctcagaacgt
ccagcccttc agcagctctc gttctgagac atgagccttg ggatgtggca gcatcagtgg
                                                                     780
                                                                     840
gacaagatgg acactgggcc acceteceag geaceagaca eagggeaegg tggagagaet
                                                                     900
tetececegt ggcacgeact tggetecece gttttgeeeg aggetgetet tetgteagae
                                                                     960
ttcctctttg taccacagtg gctctggggc caggcctgcc tgcccactgg ccatcgccac
cttccccagc tgcctcctac cagcagtttc tctgaagatc tgtcaacagg ttaagtcaat
                                                                    1020
ctggggcttc cactgcctgc attccagtcc ccagagcttg gtggtcccga aacgggaagt
                                                                    1080
                                                                    1140
acatattggg gcatggtggc ctccgtgagc aaatggtgtc ttgggcaatc tgaggccagg
acagatgttg ccccacccac tggagatggt gctgagggag gtgggtgggg ccttctggga
                                                                    1200
                                                                    1260
aggtgagtgg agaggggcac ctgccccccg ccctccccat cccctactcc cactgctcag
                                                                    1320
cgcgggccat tgcaagggtg ccacacaatg ttttgtccac cctgggacac ttctgagtat
gaagcgggat gctattaaaa actacatggg gaaacaggtg caaaccctga aaaaaaaaa
                                                                    1380
                                                                    1440
1490
```

<210> 60 <211> 1336 <212> DNA <213> Homo sapiens

<400> 60

ggcacgaggt ccagccaagt tatctaccct caaattctgg actaatcatg tttgtgcttt 60 gggtatttaa aattacatac atatattc tttttgccaa aaacaaaagt cttgcttctt 120 gtcaaatgat tgctaaagta gatcttacat tttttgttat tatgtatata tttatacaca 180 cccccaacac acttagtgat ttctgttatt tcctagggag cacagcttta aggctatgag 240 atacaactaa aaggageeea tetatttggt ttteeageea attattgtae teacatttea 300 ggggagaatc tgaaattcct gtcatgttta cagcaacaat ctatcattcc tggctagctc 360 tcagcctctc tctccttcca taggttagaa ttatgtcatt ttgttactta gtggccacgt 420 ctatttctga gaaagactgg ttacatttat gtggcatctc aggtatcatt aaggaaaagc cagagcaggg gtgagcagag gtcaaaacca cagacgcagc agggccattt gccgcctttg 480 540 gccgggatca caaccactgc agtctcccag caggtaggcc ttgccaagcc taaggctccc catccaatct agacagaggg gcgctcagag cagactttgc cgtagcccat gtctggtgag 600 660 cacaacaggg aatgaattgg gcactccact cccccgtctc tctggcccag ccctgaacta 720 gatgagctgc atttcatgga gcccatttta aaacctcttt ccttatgact ttgttactca 780 agtccagagt tetetgtgca ettetgetag ataaggagtg taageeetge eececageae 840 tggcagcacg ctgggccctc cccacacagg acaccgtgca gttccggggg aagctgactc 900 aaatcaacct tgaaatctca tgaaaacaaa atgacttgtc tttttatttg atagtgtaat 960 atcattttat aaatttttta gggtttttct cgttgtaata ttgtacagtt ttgcatggcc 1020 tggtgtgatc attttttggt tagaatataa tgctgacaaa tgtggatgga ggggaagata 1080 ctgctttagc ctatcactcc ttattttatt ttgtttggtt ttatgccctc agtgtcttag 1140 ggaactttat aagagateet etgetaeeaa acaatgatgt ggattetttt geaeagaaat 1200 atttaaggtg ggatggtaaa aaatgtcaca aaagactcct caccaatact ttatgttgat 1260 atcacttaat attaaccaga ctttgctgta ttgcaataaa acagagaact gttaaaaaaa 1320 aaaaaaaaa aaaaaa

PCT/US98/27059

```
<210> 61
  <211> 1705
  <212> DNA
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (779)
  <223> n equals a,t,g, or c
  <400> 61
  gaattcggca cagctttaca gtacatagga atttgagaac cacttcacag gaagagggaa
 acageceaat atttattat gtatacaeat aateecaagt gtgtgetggg gecaecagge
                                                                           60
                                                                          120
 ttacctgggg gaacaaggac tgtcgtgcat gtgagtgacg acattaatag catttacata
 ctgtacagat gcaacctttg atgatacata tatttgataa aaatgagaaa acagatttgt
                                                                         180
                                                                         240
 tgtagagtac ctgtccactt ttatagcatg agaacagtac aatcaactat ttattttgca
 gttactcatt tcagtgattg agaatttctg tgctgtgcag agagacggcc tgtaattggt
                                                                         300
                                                                         360
 ctcatcatcc acttgattct aacatgatct ctgcccaaag ttccatttct tgggctttga
                                                                         420
 tatttataat ggcgcctgct cttcatcttg tcttacgctt tccgagcaag ttcaaaccag
                                                                         480
 aaagaaaagg tgaggctaga agcccaaagt gagtgagtgt gaggaccaca aggaagccca
 ccactccaca gtagatgatc aaaaccacat cctcacgtgg gaggtagcac ttgggagagg
                                                                         540
 gtgtagtctg tgggcgtgat gctaccctgg aaaggaraag ggaaagttat gctgagagca
                                                                         600
                                                                         660
 ccaggcacag gttgaacacc gcagtcttag aaacagcaga gggaagactg cyttctcagg
                                                                         720
 tccccctcag gtgaggcagg gaacgggccc tcctcacctg agaccaaggg ggcccagcnt
                                                                         780
 tctccctgca cagctcaccc ccgaccagcc caggctccag caggagagac aagtaaggcc
                                                                         840
 caagtgtgcc tgagtggaaa atgtctggga cactgacctg tcaaaactgg cccctggctc
 actgggttcc catcaaatat agtgggggat ccataacaga gttsagagag gcaccgtgga
                                                                         900
                                                                         960
 gttccagggt catcggtcag cgaggaacaa ggagggaaag gtgtcttcct gccccttgat
                                                                        1020
 gctcaamtaa gcatctgttc cctagaaata catgtgtcca ggtcgtctcc atgggctttt
                                                                        1080
 ctttgcagat acttttatgt ggaacaacag tggcaaatgt tttcatttac tttgaatttg
 aaaatgttag ggtttcctcc acctttttat gaagtaaaag amcctgtcgt accagcatca
                                                                        1140
 tgagctggat gcaggagccc atggctgaaa ggagttaaaa cgcccagtgg tcattaagtg
                                                                        1200
                                                                        1260
 aaacatcttt tatcaacctg caaaagctgc cagcgttctc tgccaggtca aatgggcatg
                                                                        1320
 tttagaaaat aagagaagat ggctgagtat agctaatgaa taaatggttg tttctttaga
                                                                        1380
 aaattaaaca cacacagagt gtaagaggag aggatacggc cctccctgaa ggataaagtc
                                                                        1440
 emeetggaeg gtgeeetgee etegettete acattaactg eecaggaatg teatgetgat
                                                                       1500
 tggttcccgg aagggtgttt ggcaaggggc agtgtatgga gctacgtgta gaaggagaga
                                                                       1560
aatttgtgtg tggcttttgt aaattttgac cgattgcagc aattaaatag ttgattactg
                                                                       1620
tgttgattta aatacttatg aaagctttca gacaaaaata aactttcacg ttaccatgaa
                                                                       1680
aaaaaaaaa aaaaaaaac tcgag
                                                                       1705
<210> 62
<211> 1031
<212> DNA
<213> Homo sapiens
<400> 62
ctgacagtca ccgtccggaa tcccgggtcg acccacgcgt ccgggcgtcc gcgtcggcga
tccggggtct gggcgcggcg aggtctggtg tggcagatgt ggatagctgg accetectgg
                                                                         60
gtgcctctgc gttatgtcgt ttggttgatg catttggaga gaatctgtgc tctccacaac
                                                                        120
                                                                        180
tgcaggggca ácatgctttc ctggcctctt cagatcaggg tggctgttct tgggtgctgc
                                                                        240
accaaaactc cagcagtggg ctttcttcaa gtggccggct cacctcattc ctgccaagac
                                                                        300
ccaggtccgt gttctcacag tgctgccatc tttcctccgt gtgagcgtgg gctgtgcgga
                                                                        360
gatggacctc ggtgtgtgcg gggctgcgtg cactgccatc gctcccttct acacgagccg
gcgtggaccc agggctgagc tgtgaccacg agggccatcc cgacgagccg ccatggaccc
                                                                        420
                                                                        480
```

cgtgaccatg aggg agcgcggtcc ttgg gcctcmccat ccct cgaagctgac ccta cctggagaca gtgg tcagcccttt agga ttggcctgga attc ccggtkaatc acgt agggcggccg c	accatg agggctated scatce egaaactgtgagaace ettgetgegeteetgea macteacaggsteett etgettgeteetgeteetgeteetgeteetgeteetgeteetgeteetgegaat teceaggggggaatte tgaaaaaaaaa	g attgtttet g agaatgaege g acaggattga g geggetetgg e tgeagtetee e cagaaagetg g teagaeatgg	gaatgtggaa tcactctgcg tggggagagc aacaggcccg gaaggcttcc ttttttgggg	gcgtcggccg gcctggcctc ccaggcgaaa ggaccggtgg cccactggag gacggaggac tttaataaaa	540 600 660 720 780 840 900 960 1020
<211> 1589 <212> DNA					
<213> Homo sapi	ens				
-400- 63					
<400> 63	555555 barrers				
atagacteta atta	ccataa tagaaagaat	ggagaattat	tgattgaccg	tctttattct	60
tactogaacc caaa	tccaat gggaatacca	agggatatta	tttttacaga	tggttttcca	120
aatggcaagt toco	ggtaaa gacactcaag tggctt tccttctgct	gacagacatt	tttggcagag	catagatgaa	180
gctgctcact cctto	gctcag ctcagttttc	tatacttaa	gretecetee	tcttggtcca	240
catggtgggt gaaga	acgctg atctgccctg	t teacetatre	ccccccggge	gtggagaga	300
catggagctg aagtg	gggtaa gttccagcct	aaggcaggtg	gtgaacgtgt	atgragatga	360 4 20
aaaggaagtg gaaga	acaggc agagtgcacc	gtatcgaggg	agaacttcga	ttctgcggg	480
tggcatcact gcag	ggaagg ctgctctccg	aatacacaac	gtcacagcct	ctgacagtgg	540
aaagtacttg tgtta	atttcc aagatggtga	cttctatgaa	aaagccctgg	tggagctgaa	600
ggttgcagca ctggg	gttcta atcttcacgt	tggaagtgaa	gggttatgag	gatggagga	660
tccatctgga gtgca	aggtcc accggctggt	acccccaacc	ccaaatacag	tggagcaacg	720
ccaagggaga gaaca	atccca gctgtggaag	cacctgtggt	tgcagatgga	gtgggcctat	780
atgaagtage agcat	tctgtg atcatgagag	gcggctccgg	ggagggtgta	tcctgcatca	840
ccagaaattc cctcc	ctcggc ctggaaaaga	cagccagcat	ttccatcgca	gacccttctt	900
teteggagegee cage	ctgga tcgcagccct	ggcagggacc	ctgcctatct	tgctgctgct	960
toacatacaa actos	gttact tcttgtggag	acaacagaag	gaaataactg	ctctgtccag	1020
aagcctaaga gaga	agcaag agatgaaaga	aatgggatat	gctgcaacag	agcgggaaat .	
tagaaaagaa totta	gcctcc aggaggaact	caagagaaaa	aaaatccagt	acttgactcg	1140
Ctcttcaagc ctgg	egteeg ataccaataa geetee cattggeeaa	acacacacac	cgccctaatg	gaaaaatggc	1200
ccagtggcac tgtc	cataga ggacagattc	ctagagtage	gaaggagg	acaagggagc	1260
aaggctggag agtga	aatcta gggcatataa	aaccccacac	adadeceade	gagaaagetg	1320
ccttgcagct atcag	ggaaga tgaggagctt	ccttcatggc	ctactataaa	ctgagtaaat	1380 1440
aatatgattg cctto	ctacag cgctagagat	tcatatgttt	atccccattt	ttcaggtgag	1500
gaaatgette agate	gagget ceacettgtt	aaataaattg	gatgtatgga	aaaatagact	1560
gcaaaaaaaa aaaaa	laaaaa aaaaaaaaa	_		3	1589
<210> 64 <211> 1088 <212> DNA <213> Homo sapie	ens				
<100× 64					
<400> 64					
ctocctcass at	aaccg cactgaagga	gtggggagaa	gagcatacgc (caggagcctc	60
cottocotog gtgct	cccct aagtcttctt	cctcctgtgc	tgacctcagg (gtggtctgac	120
totagtassa tocac	gggga tgtggccctc	tcaggtgccc	ctacttgctt	tctgcttcct	180
Jauanag cocac	ctcca acattaacct	geedaceeca	ccccgtcat (ccctggagaa	240

```
ttccagcttt gtcgtatctc agagagggaa tctaattgtt tttggggggc aaaagaaagc
                                                                      300
 aacgtttagg tatcacttct acttggaccg catgcctttt tatagccaaa tttctgtgta
                                                                      360
 tttcgtaaat ggatttcgcg ttaatggata tttatgtaat aactagactt ctcagattat
                                                                      420
 tgtgagaagg gtcaggttgg aaggggtgta ggaagagggg tgaggggtag tttttttctg
                                                                      480
 ttctagtttt tttttttt ttgtcatctc tgaggtggac cttgtcacct gtggttattg
                                                                     540
 gggccaaggc ggactcagct cccggggaga agggcctctc tgccatttcg gtcccaaggt
                                                                     600
 gagctgacac aggcgttcct tttgggactg tggaagcatc agatgccagc actgactcag
                                                                     660
 gaacagcaag tcagggcaga gaggaggagg gaggctgtca ggatggaaat acctggactt
                                                                     720
 ttctttgctt ccctcgcaaa ctggggtctt ctctaccgaa cttcccagga tttcatctca
                                                                     780
 ccatatctgt gtgccgccc cagcacccc caccacctc tggggggccc gtgagcgtgt
                                                                     840
 gtcttcattg cctctctccc cttggcgtct gatgaccaca gcaaagcact gggaatttct
                                                                     900
 actetteatg ceteateetg cageeteggg ttegeattet etettett teetettee
                                                                     960
 ctctttccct gggattgact ctgagtggaa taccttggca catccactag gatctactgt
                                                                    1020
 ctgcactgtt ttctttgcat gactttatac gcagtaagta tgttgaaaac aaaaaaaaa
                                                                    1080
 aaaaaaaa
                                                                    1088
 <210> 65
 <211> 1256
 <212> DNA
 <213> Homo sapiens
<220>
<221> SITE
<222> (1079)
<223> n equals a,t,g, or c
<400> 65
gggacaagtc cacgtatatc gagtcctcga aggataggcg ggggaagatt cctgccaccc
                                                                      60
tgtgctctcg gtccagccgg acgtccatga ccttgggtgg caggaatctt cccccgccta
                                                                     120
teetteaagg acaagteeac gtatategag teetegacea aagtgtatga tgatatggea
                                                                     180
ttccggtacc tgtcctggat cctcttcccg ctcctgggct gctatgccgt ctacagtctt
                                                                     240
ctgtacctgg agcacaaggg ctggtactcc tgggtgctca gcatgctcta cggcttcctg
                                                                    300
ctgaccttcg gcttcatcac catgacgccc cagctcttca tcaactacaa gctcaagtct
                                                                    360
gtggcccacc ttccctggcg catgctcacc tacaaggccc tcaacacatt catcgacgac
                                                                     420
ctgttcgcct ttgtcatcaa gatgcccgtt atgtaccgga tcggctgcct gcgggacgat
                                                                    480
gtggttttct tcatctacct ctaccaacgg tggatctacc gcgtcgaccc cacccgagte
                                                                    540
aacgagtttg gcatgagtgg agaagacccc acagctgccg cccccgtggc cgaggttccc
                                                                    600
acagcagcag gggccctcac gcccacct gcacccacca cgaccaccgc caccagggag
                                                                    660
gaggeeteca egteeetgee caccaagece acceaggggg ceagetetge cagegageee
                                                                    720
caggaagccc ctccaaagcc agcagaggac aagaaaaagg attagtcgag actggtcctc
                                                                    780
840
tgtcgccctt tccctggaca gatcaggccg gggcggtggg aggcccgcct caggtcaggg
                                                                    900
cccagcgtgt gacgtagggg ccggggcagg ccagggtttg tttgtggagg cgctgtctgt
                                                                    960
ccctctgtcc ctctgtgttt ccagccatct cgccctgcca gcccagcacc actgggaatc
                                                                   1020
atggtgaagc tgatgcagcg ttgccgaggg ggtgggttgg gcgggggtgg ggccgggcnc
                                                                   1080
ccctacggga tgcccacggc cgttcatcat cttgtccctc gtccccctac cacactcccc
                                                                   1140
ctcctagacc gccgcccttt aacacagtct ggatttaata aattcatatg ggtgtttaac
                                                                   1200
1256
<210> 66
<211> 1602
<212> DNA
<213> Homo sapiens
<400> 66
```

ggcacgagaa aacctgtgg					60
gatttgagtt gggatgaca					120
tttctcccca tgtatgaat					180
agtggactta tgtgcctcc					240
cgatgcttct gctggattc					300
gttctgcggg atccagggt					360
tccaccctgc gctggtcct					420
cctctcatag gcagccctc					480
cctgggacct gtgcttcca					540
cctctgccct ttggtgacc					600
atcctcccgc caggtctgt	a gtctctaccc	ggtcacccct	tcttcctggg	accatgcccc	660
agatcagetg ctaccetea					720
actgggtgcc accttctcc	c ccatcatcac	gctcactgct	ttctcttgat	gggtaaggct	780
tcccgaatga tgggaacta	a cagtggtggt	gaagtcgagg	cagacttcat	caggcattta	840
gcatccaagg ggtggctca	t gagtgcagat	acagtgcagg	ggccggagag	gggctgggct	900
gggctgacct gggaggctg	a ggctgatgga	gagtgggcag	gtagggtgga	gaggcaggaa	960
ggttggtggc agccacatg	g ctgagggcta	gagcctggcc	agggagtctg	gagagaggca	1020
gtgggtgggc tgggggttc	a gcctgctgaa	ggggagcact	ggtcagtgcc	cataccccat	1080
ggggtgaagg cctgggcag	g gcccaggggc	agcttcgagg	gtgacctgga	gctgctcagg	1140
aagtgagatg gcccagcct	g acctgaccat	tggctggcaa	ggaacgggat	ggagaagttg	1200
tgtcctgggc cttcagcga	g tgtgacattg	tcattgttgg	gatagcttta	aagatctgat	1260
tgcttatgac atgccttgt	a gcgctaccag	catcttggca	tttggcaggt	ctagtccagc	1320
tcgctgtttg cacgtcttc					1380
tcccccatt gatgggagg					1440
aggatagttt cattctgat	a gtttttttt	tttttttt	ttggagactg	agtttccctc	1500
tgtcgcccgg gctggagtg	c agttgtgtga	tctcggctca	ctgcaagctc	cacctcccag	1560
gttcatgctc gtgccgaat	t cgatatcaag	cttatcgata	cc		1602
<210> 67					
<211> 938					
<212> DNA		•			
<213> Homo sapiens					
<400> 67					
ccacgcgtcc gctgccagc					60
ccctcggaaa gaacggata					120
ggtgtggcac cggtgcacg					180
catcgctgga cgctttgtg					240
tcttttcctg gacagtgta					300
ataaaacaac aactcatgt					360
agaaatctcg actctatca					420
cagagactga aggcactct					480
ctggacggtt ctgtggtta					540
tgtttctgct gttggctac					600
atacttttgt gataaaaa					660
aaatataata aaaataaaa					720
gaggagcagt cctatgctt					780
tgcctttcct tccttctgt					840
aaacattgcc aacgcaaat			aaaaaaaaa	aaaaaaaaa	900
aaaaaaaaa aaaaaaaaa	a aaaaaaaaa	aaaaaaa			938

<210> 68

<211> 1585

<212> DNA

<213> Homo sapiens

```
<220>
<221> SITE
 <222> (904)
 <223> n equals a,t,g, or c
 <400> 68
 gggttgctgt tggggtgtgt cgrgaggacg tcatgggaat tactgatcgt tcaaaaatgt
                                                                          60
 ccccagatgt gggcatctgg gcgatttatt ggagtgctgc tggctattgg cccttgatag
                                                                        120
 gcttccctgg aactccsacc cagcaagagc cagctctcca ccgagtgggg gtttacctgg
                                                                        180
atcgtgggac tgggaatgtc tccttctaca gcgctgtgga cggagtgcac ctgcacacct
                                                                        240
 tttcttgttc ttctgtctca cgcctccggc catttttttt ggttgagtcc attagcatct
                                                                        300
 ttagtcattc caccagtgac tgataggaaa tgaggctttt cttcccctga ccaaaactcc
                                                                        360
 ttccctgtag tccagctgag ggacacacat ccctgggccc tcttctgccc ttcatgtctc
                                                                        420
tatectggat ggtecatett etgggtetee etaaeggtae egtttggtat etgecetttg
                                                                        480
 tgtgcttcac aagaggcagt cccatgggag gtgggtctgg ccaatggaga tgggacagga
                                                                        540
aattttccaa gacgcttttg ggaaatcttt ttgtagcttt taaagagatg tgcggggaag
                                                                        600
acatatggat gttagcagcc atattggaac tgagaacaca ggaatggtgg aaaggtagaa
                                                                        660
gaaacagagt ttttgttgcc gttgtgaaat tgttgaaatt tccttcatgc caagcttctt
                                                                        720
gttatatgag ataattacgc ccttattgta taagacaatt ttagttgtat ttggttactt
                                                                        780
gcagcctgaa gtaccgtaac trcactaaag ggacgtagtg tgaacatccc gcagtatagg
                                                                        840
cttaagtcac ttttgtgaaa tttgacaaag gcatagatct ttttctatcc agtcaggcat
                                                                        900
tgcntattct ttccagtaac tactgattcc cccacttttc tgtcttagaa aattgtggga
                                                                        960
attccccctt actctgccta tgttgcactc tctctctcc caaccataac tctgccctca
                                                                       1020
gctattaact gtgctgtgta tttatcaagt tggtatgttg tatgtacagt gttattcatg
                                                                       1080
tcatcatgag aatgttgaac gcttgttaaa tatcttttgc tagcctcttc atatgctgtt
                                                                       1140
gcatatgact ctcatcacaa ctcagtgaga tggaaagtca aatcctattt gtacaaatga
                                                                       1200
gaaaactgaa ctctttagag taactagctc agtattggcc agctggtaaa tggcagtgtt
                                                                       1260
gggattaaaa tccagttctt atctactctc cctttattca gaagcattta ttggatgttg
                                                                       1320
atctttgttt caggttttga ttttgttact tttttatact gtgtatattt tcctcagtct
                                                                       1380
accettetge tetagattgt etggaeteag gagattgtgg eagttactgg atagttattt
                                                                       1440
ttaagataat gattgctttt ctctgtttat ataagtcatg tgtacttatt gtagaaagtt
                                                                       1500
tgtaagatgc aaaaagtata aaaattaaag ttatgcacta ctaaaaaaaa aaaaaaaaa
                                                                       1560
aaaaaaaaa aaaaagggcg gccgc
                                                                       1585
<210> 69
<211> 1676
<212> DNA
<213> Homo sapiens
<400> 69
ggcacgaggg gacttcagaa ccacagaact gagatgataa atgagtggtg tttcaagttg
                                                                         60
ctaagtttgt ggtcatttgc ttacagtaat tgtaaactaa tacacaagtg taagtttgtt
                                                                        120
ttcttaaaga agaaaaaac ggggaaggag gtaagtgtta aaggatcaaa actctgacaa
                                                                        180
aaggctggtt gcagaacatg acaggttgtt gcactggaaa ctatttgtca tgcaagttta
                                                                        240
tgttaaaata agtagctttt gaggactttc atttttggtc ttgtaaacat gccatttaat
                                                                        300
attgtccmac tgataatact ttttgcaaac agaaactgtt aaaaccttta aagcaaatat
                                                                        360
tactgtagag aagaagtaat gtgttatgaa actgtgagga tactaagaag gatcctactt
                                                                        420
aagtttette ageataaata aacttgageg tttegaceae tgttaetgag aatgaaatta
                                                                        480
tttcttaatc acttttaatg aggtaaaatt tacatacgat aaaatgcacc aattttaaag
                                                                       540
tatagtttaa tgagcttgca cagatgtaaa tatctgttta acttctactt aatcaagata
                                                                       600
tagaatattt ccacaatgcc aaaattgcca ttgaccccct tccccttctt tcacccaact
                                                                       660
gcagacccca ggtcaccacc aacctactct tgctcaatat agatttaatg tgatgtgtct
                                                                       720
tttctagagt tttatgtcaa tagaattgta cactatgcac tcttccatgc ctggctttct
                                                                       780
ttgctcagca graggtgttt agattaattc agtagttcat ttctttctag taatgaatag
                                                                       840
gatcacatta tacattatac cacagagtgt gcatccatta ctttgtkgat tgatatttgg
                                                                       900
```

			36			
gtcatttcc	a ggttttggc	t attgtgaat	a aaactgcct	t gactattcc	t gwacaagtct	960
regratia	y gaacatacgi	t tttattttc	t cttgaggaa	g ttcctagca	a taagartger	1020
gggccacac	g gtaggtatai	t atttagctt	t aaaagcaac	t aagtgcttt	C Caaagtgact	1080
gracaattt	a acattectad	ctgaaatgt:	a agagaattc	c agttgctcc	a cattettete	1140
aaccccttgg	t agcatcagto	: tctttaagaa	a ttctaatgg	a tatotaata	t ggactatagg	1200
cctaattig	c atttctctgt	t tgactaatga	a tgttgcaca	a cttttcata	t ofcratcasc	1260
catteringe	a cottettta	a tgaaatgtc	t gttcaaatc	a tttqtccac	t trrrattoto	1320
CCallitati	cagttgtaag	g agttctttad	c atattctgg.	a aacaagtee	t ctotcacata	1380
Lataygtact	tigaaaatct	gtgctttgc	tttacattt	t tttaatggt:	actttttaac	1440
agragaragi	- cttggttttg	, atgaaattca	a acttatcag	t ttttcagtta	a tagtatgtar	1500
ttttatgaco	catctaagaa	gcatctgtct	acccagagt	t gcaaagatai	cccttttctt	1560
actagaaata	ttatagtttt	atttaccatt	gcttctatga	a tacatttaa	gttaatttt	
gtgtattaaa	tgaataaaa	gttgaagtto	: aaaaaaaaa	aaaaaaaact	Cutado	1620
					. cgcagg	1676
<210> 70	•					
<211> 1344						
<212> DNA						
<213> Homo	sapiens					
<400> 70						
ggcacgagcg	ccagataact	caactttccc	attggctacc	tttaaatcea	atastat	
ctagacctat	cgcctatgcc	tgatggtggg	tcacataata	casstattas	grgateteca	60
agtggattag	ggatgtggct	gggctcatgg	ttgacgtccc	tactactac	ctgagagett	120
tcaggctggg	agaaggtacc	atgttgtgtg	actootcate	tgctgctgag	cccttacggg	180
ttgctgggct	tggcaggtgt	tcaaagtgac	Catttetete	aggreett	cagctgttgc	240
tcctcagatg	tactccctg	adaccascaa	tettteette	aagggtttt	ttctgagtat	300
cttgcttgtg	aatgtttcct	tcatctccag	attatata	cacagggcga	tgcttcccta	360
gcctgggcag	gatttacaga	agactaceta	getgeetggg	gacaattetg	tcttttggag	420
tgtagggtaa	gatttacaga	attrators	tagtette	cctgccgggt	ccacttctgg	480
gtacagtttc	acacctgccc	tttttagg	caguguugat	agaataatca	ttttctttca	540
ttctcgagct	ctttttttt	22000000	cagettttta	gatgtagcac	ttaatgccag	600
gctctctcac	ccccaaactt	aayyyacaca	ggtcaacaag	cagtaggtct	ttggaagctc	660
taggagaaaa	atggtataag	grgagggga	cacatggaat	gtaaacctcc	aaactaatta	720
attaaaaaca	aggaatgaga	aaaacaaaca	caagaaggca	aaacaaaaac	acctggttca	780
Caaaaaaatt	acaacaaagc	aaaacaaaaa	aaacccaaaa	ccaaaccaca	caataaatga	840
aattccaaat	acataaaaca	gatgacatgt	atagaaataa	aaaaatagaa	tggaggaact	900
acactggatt	atataagtaa	tcctaagtgg	actaaatttg	caaagtaaaa	ggcaaacatt	960
aaaacagata	aaaaaacaaa	ccagggaat	acagttcaca	gctgatacat	tcaaaatata	1020
taggaggeta	aaatataaat	aaaatcggta	cagtggtgtc	tgcctgtaat	cccagctagt	1080
aaacaaact	aggcaggaag	accccttgag	tctaggagtt	agagaacagc	ttgggcaaca	1140
acacacacac	gtctctaaaa	aaatacacac	acacacacac	acacacacac	acacacacac	1200
Cdadatcdcac	acacacacac	acacacacac	acacacacac	agactgaaat	ggaaatgagc	1260
aaaaaaaaa	ccactgcact	ccagcctggc	aacagagtga	gactctgtct	caaaaaaaa	1320
aaaaaaaaa	aaaaaaaaa	aaaa				1344
<210> 71						
<211> /1						
<211> 14/4 <212> DNA						
<213> Homo	sapiens					
~400s 31						
<400> 71						
ygcacgagct	aaaatatgct	taaagtaaga	tgtttctatg	ttatgtggtt a	atgttatcaa	60
caacacccgg	tigatettea (catattttat :	atgcatatat a	atatcaagaa d	ittatatata	120
LaLaactcaa	gaaactcaag i	ttatatatat a	atgtcaagaa a	atotatoarr a	atttagaga	180
gaargggccc	aaatgtgaaa a	aagatataaa a	aaaacaaaa a	aaaacaaaaa a	aaaacacta	240
ttttccccta	cgaaatatac 1	tgtatatttc a	aaaagaagaa a	aagttaaaag a	tatttgaag	300
			=	- 5		200

```
attgcagggg caaaacaaaa acctaccagg gctcagcact taagcacttt tcccacatcc
  agggtcaaag cagcagtaac tacatggact tttaagtgcg gtatgaaatg caacattacg
                                                                         360
  cttacaaaca gtactgtcaa acctcaaatg ctttctttct tcagatgctt tttcgtgtac
                                                                         420
  atgatactag tagacacttt tctctttata tttactgata gtgaaaatca tacgcaataa
                                                                         480
  aatattgatg tttgaaggca gtggtcacca attggttaaa aaactatgaa atgtaaactg
                                                                         540
  aattgttata tetetateet ttttgetttt etetgtgttt ttaatgtatg gaataaatet
                                                                         600
  cataaataga aagaaaaata atctagaaat ttttcaaagc tagtactctt tctccttata
                                                                        660
  aatgtacaca attttaatct ttttacaaat ttatttaact gtacctactg tacttattgt
                                                                        720
  agattcaatg acgcagttaa gtcatcaccc aaggatttat gaatttgaga ttactgacct
                                                                        780
  gttttcttca tattgcattc acatcaatat ttgtgaattt gttgttcagc ttttcattca
                                                                        840
  aacaaaaaat attccctcaa gaaagctccc tttttatcat aaacatttca acttacccaa
                                                                        900
  cattagaaca agtctgccat gttaaaaata atttaaagac ttatctctga aaacggtatc
                                                                        960
  cagaaacgca ggtgttccca gtaatgtagc ttcaaaaata aaatgtgcta tttatatgac
                                                                       1020
  tgaaattcat aacttttgga agggtatatt tatgacagca taaaaaataa attctgtgct
                                                                       1080
 ataaagaaga tccaacaaat taaccatata agcacagaaa gtagagaaac acagttattg
                                                                       1140
 aatctactct tgtcattaac attttcaaaa aacaaaatgc atattgtaat atttggtaca
                                                                       1200
 tgacacttgc atgttgatat gcctatatac ttacaaagta ttcaatgtgt acttagcggc
                                                                       1260
 gcttaaaata tgtcatgtac aactcttata aacattttta cagggttccc atttgcactt
                                                                       1320
 catctttcag taaagtcttg tcagaaaaaa attgtctgat aaatatggaa aaataaaatt
                                                                       1380
 tgaattttag ttaaaaaaaa aaaaaaaaaa aaaa
                                                                      1440
                                                                      1474
 <210> 72
 <211> 2012
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (1468)
 <223> n equals a,t,g, or c
 <400> 72
 aattttttaa aagcaatttt aggttcatag caaaatttag cagaaagaac agagttctta
 tataccettt etgettttee ecaageetet tgeactaata aegttetgta ecagagtggt
                                                                        60
                                                                       120
atgtttgtta caatcagtga acctagactg gacacctcat tatcacccaa gaccaaggtt
tacgttaagg ttcgctctta gtgttgtata ttctatgagt ttgacaaatg tttaatgaca
                                                                      180
tgtatccacc atgatagtat catacagaat agtttcactg ccttcctctg tgctctgcct
                                                                      240
gttcatccct cccttcctgc tgatcttcta ttgtctccat agttttgtct tttcccaaat
                                                                      300
gctgtatagt tggaattatc atgtaacctt tcaaatggcc ttttcactta taatatgcgt
                                                                      360
ttaaggtttt ctacagtctt kgcaggcttg atagctcatt tttctttagt gctgaatact
                                                                      420
attccattgt ttggatgcat tacagtttat tcattcacct actgaaggaa atcttgcctg
                                                                      480
cttccaagtt ttgtcaataa agctgctttg taaacatcca tgtgcaggtt tttgtgtgga
                                                                      540
cataagtttt caactcattt gggtaaatac caagcagcac aattgccgtg ttgtatagta
                                                                      600
agagaatgtt tagtttcata agacatcacc aagctgtctt acaaagtggc tgtactattt
                                                                      660
tgcacttcca ccagcaatga atgagagttc ttgttggttc cacatactcg tcagcatttg
                                                                      720
atgatatcag tgttttagat tttgaccatt taataggtgt gtagtggcat ctccttgttg
                                                                      780
ctttaacttg taattctcta atgacttata atgttgagca tcttttcata tacttatttg
                                                                      840
900
acagggtatc actctgtctc tcggactgga gtgcagtggt acggtcacag ctcgctgcag
                                                                      960
cctcgatgtc ccaggctcag gtgatcctcc catctcggcc tcctgagtag ctggaactac
                                                                     1020
aggcacatgc caccatgcct agctaatttt ttatattttt agaagagaca ggtttcgtca
                                                                     1080
tgttagtcag gctggtctca aactcgtggg ctcaagtgat ccacccacct tggcctccga
                                                                     1140
aagtgccggg attgcaggca tgagccackg tgcccagcca atcaaatgag aaaagggcag
                                                                     1200
tctcttcaac aaatggtgtt gggaaaattg aatatccaca ttcaaaagaa tgaaattaga
                                                                     1260
tgcttacctt aaactgtata caaaaattac ctcaaaaaag atcgaagtcc taaatgtaag
                                                                     1320
acctaaaact ataaaactct tagataaaaa cataggagga cattggattt ggcaatggat
```

```
ttcttgggcg tgacaccaaa aacaggcnac mgaagtaaaa atagatggat gacatcaaaa
                                                                       1500
  tttaaaactt ctgtgtatca aagaacacat tcaacagagt gaaaaggccc ataaaatggg
                                                                       1560
  tgaaaatatt tgcaaatgat atatcctgta agaggctaat atccagaata cataaggaaa
  tcctaccatt caataacaaa aaacaacctg attttaaagt gaagaagtca agaaaataag
                                                                       1620
                                                                       1680
  atagactaca tactgggaga aaatatttgc aaaagatata tctaataaag gactgttatc
  caaaatatac aaaagaactc taaacgataa gaagacaaat agcctgaata aaatacagca
                                                                       1740
 aaagacttga acacataccc cactaaagaa gattcacaar rttgggtgca gtggttcgcg
                                                                       1800
 cctgtaatcc taacactttt ggaggccaag gtgggagaat cgcttgagcc tgggaggtcg
                                                                       1860
 gggctgcagc gggctgtgat tgtgmcgctg cactccggcc tgggcaacag agggagaccg
                                                                       1920
                                                                       1980
  tgtctgaaaa aaaaaaaaa aaaaacctcg ag
                                                                       2012
 <210> 73
 <211> 1267
 <212> DNA
 <213> Homo sapiens
 <400> 73
 ggcacgagct cactctagct gctatgataa acaagaagac cagtgaggaa gttttgaaac
 tetectetge aagagaatgg tggecageea ggegtggtgg ttgtegaate tgtggeacet
                                                                        60
 gtgggaagtg ggctcagccc agggactgcc tttggatccc ccagcattgg caccatacct
                                                                       120
 accotgggcc ctaaggtggc catgottoto tggatttgct toootagcag gggototagt
                                                                       180
 gettgeecac teeetgeeca cageatggee tgggageage tgagaetggg ggeeagetea
                                                                       240
                                                                       300
 tecegegteg attectggaa gtgttateag tgeetgttat ggaggetgga eccatgagtg
 gcagccttcc ctggcagctg ggctgacctg tctgcttttc cattgctcgc tggttttgtt
                                                                       360
                                                                       420
 cactgtaggg cgtgaggggt gagtagctgc tggcctccaa gtccatagct actcatgttg
 tacgctgttc acagggacct ctaaggatgt acatcatcac acattcacac acatgcacca
                                                                       480
 ggatttgctt tttttggcag cttttccctt cctggcttcc tttttgagtg gtggaagtaa
                                                                       540
 aataaaaagc aactagggct gggcacagtg gctcacgcct gtaatcccag tacttttaga
                                                                       600
 ggctgaggcg ggcagattac ttgaggtcag gagtttgaga ccagcctggc caacatggtg
                                                                       660
 aaaccccgtc tctactaaaa atacaaaaat tagctgggag tggtggtgca cccctgtagt
                                                                       720
 cccagctact cgggaggcta aggcaggaga atcacttcaa cctgggaggc ggaggttgca
                                                                       780
gtgagctgag atcacaccac agcactccag cctgggtgac agagccagac tgtgtctcaa
                                                                       840
aacaaacaaa caaacaacaa caacaacaaa aaactgggct ctggtggttg ggaggaggag
                                                                       900
ggaaggaagc aagtaccagg gtaagcagga tggatggatg gctctccccc agaggggcgg
                                                                       960
cagcacacag agttctggag tcagactcag tagagggcca gttttgactc cactgccaac
                                                                      1020
cacctggctg actccaggca ggttacatca ctgatgaaag cctcagtttc cttgtctata
                                                                     1080
aattgggggt acaagcgatg aaaagaggct caacatcact aatcactagg gaaatgcaaa
                                                                     1140
                                                                     1200
1260
aaaaaaa
                                                                     1267
<210> 74
<211> 1748
<212> DNA
<213> Homo sapiens
<400> 74
ggcacgagta aagacaaaat aaattettet gtecaettat ttaeetaaca tacaettget
                                                                       60
teettggaag teataggeat ecacatatet teagecacaa ettggtattt etaatataat
tottattttt gaactootaa actttotggt agaaatotto agttgaaaat atootggcaa
                                                                      120
gtaaaattag aaactcccag aaatgtactt atttctatta tgttgtttta tttctgaaca
                                                                      180
ttgtgcccaa cattctttc cacatacttg cccaaattgg aaaactaggg ttctaagttt
                                                                      240
ccccctccat ccatgcccac atttaattca ccctaataat acctgacatc tttcaagttc
                                                                      300
attttctact atctatcccc acgcaggcca tatctgggtt gaagcttcat tatctctata
                                                                      360
gattaaaaac aaaaacaaaa tgcatacaag caaaacaaat aacatacaaa caaaacccac
                                                                      420
ctaactcatc tttatgtagt cagtcctccc tcaatagttt ggccaaactt cctaaaccga
                                                                      480
                                                                      540
```

```
aatctgattg tgactatccc cttctaaatg tatttaatca gcatacccct tcaataaatc
  cattaaccgt tcttgttatc caagacagtt tgtcatctgt cttggataac aagttgcaga
                                                                        600
  ctccatccaa tgccattttc ccctagaaat atagataatg gcactatagg aacaatgatc
                                                                        660
  tocacatgoe toatgoattg graatttttt taacetttge tagaaatgtt etgetecact
                                                                        720
  ctactcatcc accacccatt ctactccacc ttacactacc tcttttccca tttagatctt
                                                                        780
  ccattctata tctccttgca tgaaattgtc catacctgct tagtactcat ctcattattt
                                                                        840
  tgtcattgtg cgcatatctg ttcatatgat ttcttatgga agttattaag tattttgatt
                                                                        900
  tctgtttcag tcagatttcc aacagagaag tagaaccagt agaaaatata tcttaagata
                                                                        960
  cttattggag ggaattaact tacatggttg tgggaaccgg catagccgac ctaaaattta
                                                                       1020
  tatggctgac tatcaaaaaa gacaggctgg aactcttagg cacaggcaga agttgcagtt
                                                                       1080
  cacaggtgaa atttgttett tateetggaa geetgggete tgetetttag atttageage
                                                                       1140
  tgactgaatc aagtccacct agattaccta ggataatctt gtttacgatt atgattatca
                                                                       1200
 ctaccagtta tcaactgatt ttgaacttca ttcacatcta caaaatacct tcataggaac
                                                                       1260
 atctagatca gtgttggatt aaataactat cagctgtagc ctagccatgt tgacccatca
                                                                       1320
 aaagaccatc acaattgctg atataacttt aataaaattt gcaacatttt cagatggaag
                                                                      1380
 aattgagaaa agggaagcgg gctgactttt cattttagaa tttattatgc attaacttaa
                                                                      1440
 agtaagtaat aattatgtag gtgatcattt tgatatttta acctacttaa tttagaaaat
                                                                      1500
 catttaaaat catttttgtt aagactacaa aatgattttg ggtaaaaaaa aattttacca
                                                                      1560
 aatatcaaga tcacaataat cacttaaaat agttacatat gtaactaacc tgcacaatgt
                                                                      1620
 1680
 aaaaaaaa
                                                                      1740
                                                                      1748
 <210> 75
 <211> 1570
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (7)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (8)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (10)
<223> n equals a,t,g, or c
<400> 75
taccggnnan ggaattcccg ggtcgaccca cgcgtccgat tttatgctat ccagtwttta
cgtacccatg tgtcaacatt tcatatatcc agttctttgg gtgctggttc acttttttc
                                                                       60
atttattcaa attcagaaaa atacggacgg atctaatgtt aaattaacca gaaaccctgg
                                                                      120
aacattcata tottgagagg gaatttgota otottttaot tttgggattt cattataaaa
                                                                      180
taggeteatt ttatacatat gteetgtggt etgtetteea gagtgtgetg taatcataag
                                                                      240
tctctagcaa agagtggagg gtggagggtg tgtagaactc cactcagcct catggataca
                                                                      300
totacaagto totcaaccca tootgttaca gttotccatg agagtcacct cacacttgga
                                                                      360
aaagaaggag gtttaaagca gagtattgtt ggcagccagc tatgcccatc ctcttgtaaa
                                                                      420
taactttcca acacaccat ttccttgcct taaggtgcag gttcctactt ctacaaaatt
                                                                      480
tcaaatgatt gcaggtcaaa aacctttgga gttactcaca aataataata aaatttcaaa
                                                                      540
taactagggt ctacttgtcc atcaagatga cattaccagt ggaacccacc tgttaatttt
                                                                      600
aaagtagett cagaacecaa caaaaattat gtaageetgg ttaaatgtee ttttttette
                                                                     660
ttgcctctaa taraatcagg atcttcggcc ttgatactaa atatgtgtat atttagttat
                                                                     720
                                                                     780
```

~~ + ~ - + +			40			
gatggtact	t gtagatget	c acatttcca	g ttccaaact	c gcccgtact	tt tttatgtgct	840
	r ggacacact	L CIGITALE	ic atgatttet	o tatocaca:		
- councide co	u gicaatta	y aagttaatt	T ccaatctac	it ctcaactor	ataastus-	
ugg caa	u ucaaytaaa	L yagtttggd	ia cattttgad	ia ttaatotts	c teasanne	1020
accyccuac	L LLadalggc	c cctaatgca	la ccaaaatta	it aaccaate	2 002+0+	
gaaaggtat	L LLLaallati	taaaatcat	t ototatarr	a cadcadtat		1080
ggccaaaga	y yarrılıla	a aagatgaag	a atggtttt	ic ttatattat	a tammete	1140
gageeegeg	a yeayeataa	aacaatcat	t ccttaatto	t teattere	(2 30tman===	1200
cccgnaac	y callillia	ı aaggagact	C Ctagacaca	d cydtaatao	a aaaata	1260
egeagagee	L LLCLCalaa	: acaaaacca	g aaaataatt	t tragractt	t asatts	1320
atgtaataag	g gaaaaaaatt	gtttccaca	a agtrgaact	a totageace	a tttggtaaca	1380
tatggcatgg	g ccactttata	tcacagaat	a tatatasa	t tacaaaaa	t acttgggcca	1440
tagtagacad	taagaattaa	aactcttaa	a tractores	c cycaaayca	a aaaaaaaaaa	1500
gggcggccgd	3		u ccagcgaaa	c aaaaaaaaa	a aaaaaaaaa	1560
						1570
<210> 76						
<211> 524						
<212> DNA						
<213> Homo	Sanione					
120 1101110	saptens					
<400> 76						
		6366666				
tgcagatctg	tratector	cacyayacg	J cctcccctc	gccctgcggt	cccgcgcgga	60
accountate	ttggacccagc	gragcarcto	f tagcagctgg	g gacatcatto	ceegegegga caggttttgg	120
239-9-9	ccyycaacaa	Ciggateta	l agatggcagt	Caddataatt		180
uguc cgc c	ccgagtgctg	rggtgtctcc	: ttccgcagac	' agactatata		240
-90000000	gececcigag	grgatggcad	i qtaaaactcc	· acatatata	. atas====	300
gougeaga	geergeerga	yaagctgacq	i ggagaettta	t taaaaaaaaa t	atamant	360
-333 cagacg	aytaytaaat	ccacaagcag	agcagcagcc	* tctctctctc		420
	ggacticata	retecttee	gagtggtgac	actoacette	tgggtaatgc	480
taataaacca	ccagtctctt	tgatgtaaaa	aaaaaaaaa	aaaa		524
		•				324
<210> 77						
<211> 1306	•					
<212> DNA	•					
<213> Homo	sapiens					
<400> 77						
gaagetegaa	attaaccctc	actaaaggga	acaaaagctg	gagctccacc	geggtagaea	60
	3 cag cgg	accelegge	CLUCATORAL	TCGGGGGGC~~~		120
	CCCCCacaa	yaaytaccta	gatagggagt	CCCSCCSSCS	~~~~	180
Jungaccc	rgccagcagc	rerectiace	agggagteta	Catogototo	***	240
	ccagtacggc	caccttctat	tteettette	Ctaggtggg		300
	ccaagggccc	cccaggcaag	gagaatagca	Cttcataaaa		360
-g-coogag	ggrgrgrggc	cctatactac	gcccattgca	atctctcaca		
	ceggegeegg	cctgcgagga	atggtgtgct	Cacactatas	~~~	420 480
33-00000	Lettggggtt	gctgctcttc	Ctcaaggarg	tttctccc		540
	ecceoggic .	cacaaaggac	agaatatota	tectasses		-
acgaa	urgryrgry ,	ctgtgcacag	accectecet	ccatatact-		600
JJauagg	acceactatt	adididiti	EEgagatoto	CECSESSES		660 730
	cccarggarg .	Luuccaaucu	Egaaatcatc	tataaatt		720
_50000000	crygaygicc (cctggaagee	agtgtttgct	atatataaaa		780
	egaggeetge (Cactected -	aaaatatctc	22222++~+		840
	gguvaataty (ACCLECCCCC	aagcactgcc	20t000		900
3 TTTTTT	guugayetat (Jugaagetgg	adaadaaccc	202022002		960
gggcccggct	tcagaggtac t	ccttgtcac	tccagagaga	-yuyaayyag aaacttaaa	yayyagcact	1020
	-	<u> </u>			aayugaggct	1080

71	
gccaccgccc tgggatctct gaaaaggagg tttcagccac gaggcagctg cttccaggac	1140
a sa a a a a a a a a a a a a a a a a a	1140
ggcctctgca gaaccagcaa ggggaaaagt ataatctggg ggaccttcaa ccactaagcc	1200
tettgteaga acceteagge agggeagatg tgteaceaaa taaaac	1260
os ossetated tyteateaa tadaac	1306
<210> 78	
<211> 1479	
<212> DNA	
<213> Homo sapiens	
<400> 78	
acgsgaaget egaaattaae eetcaetgaa agggaacaaa agetggaget eeacegeggt	60
as sostas decagaacta gradalcccc caaactacaa asstrant	120
The state of the control of the cont	
situation decodately dateleacte anactatant through the	180
The same of the sa	240
The state of the s	300
totcagttta ttottaaata tgacccaact ccagcettta toccaattta tactacctet	360
gtcctgattc aaggettcat tatotetese ctageettta tcccaattta tactacetet	420
gtcctgattc aaggcttcat tatctgtcac ctaaatgtac ttgaagctgt agtgccctgc	480
The state of the s	540
The state of the s	600
SSTEET WOODGALLYA YAAACILLOCA AFCTACCAGA AFCTACAGA	660
33-3-4 waageceec acqaeeedar FFFAcFFFFA AFAFFFF	720
Jarran Congregation Calledadaa Cacactetet tactus	780
o o o o o o o o o o o o o o o o o o o	840
ctttttttg tggcagctgt tattgcactt tgcaacattt gccaaaacgt ttctgactcc	900
Ccaqcctqtt ttataqtaac actqtatatt tgcaacattt gccaaaacgt ttctgactcc	960
ccagcotgtt ttatagtaac actcatatgg acaccttgaa aatttataaa atattattc	1020
	1080
T JETT JUSTICUADA CLAULADATE FEFSTAFFES SSAFFELL	1140
o bullet a management of the contract of the c	1200
Today Colude at a second colude at a constant at a constan	
The state of the s	1260
To 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	1320
tgagtaactg agactcctat ctcaaaaaaa aaaaaaaaaa	1380
gggtacccaa ttcgccctca tcagtgcagt cgtattaca	1440
o was considered to the constant of the consta	1479
<210> 79	
<211> 1794	
<212> DNA	
<213> Homo sapiens	
<400> 79	
ggcacgagaa gcatttagta ggattttaaa gaaacttgag aactgttaca taaggtgatg	
aattgggcat agcatgtaaa attatattta agcaaggaaa tgatctctgg tgttttaata	60
ttcaacttga ttgcttcctc ttggsttcta dyddaggaaa tgatctctgg tgttttaata	120
	180
344CCCCCC CUCALCAFFF FFCCaffaaaa LLL_L.	240
J-JJ- WJCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	300
	360
-55-Cyccc clackuctur arrottate and	420
	480
tggtacagtc tgcttactta aaaggtgagg cttgaattaa aatacagcca gatagaagcc	540
agactctaat caaatgaggt cattagatga of	600
	660
tgcctttccc tggctgttga atagctgatg ttccagattg ccctacagtg ttgtgttagg	720
- 235	. 20

```
gcatccagga gggatacttt tcaggcttag gtacacctca gtctttaaaa tgaggaatta
                                                                        780
  ggacacattc atgtgtgtgt ccctaatctg ctcctgagaa gagaagtgca atcagggtct
  tattttgtga ccactgactt gcacactgag acaaaaggge catctgcaag ctgaaaatag
                                                                        840
  tggattcctt aaataaaaac tattcacatt tgatggtgtg gtagttttaa taaaatgttc
                                                                        900
  aagtgtcaag ttcattttca tttataatct gagacagttt tataagtcac ctccctgggg
                                                                        960
  gtaaaaatgc atgttctgtc ctcatagtga gacacatctt ctgcttagag tctagaaagc
                                                                       1020
  tctaagaaag atttatgcca tctgtgcagc tggcattttt atagtaaaat ttttttact
                                                                       1080
  ttgctccaag tttaagttat ctcatgacaa actttcttga aagaggcatt cactattatt
                                                                       1140
 ataggaagta tacttcttta ttgaaaagga gataatgtat caggtaactt attaaagtat
                                                                       1200
 tttctcaaag tttagtatct ttaggaatac agtgcctcaa tacaatataa aatatttgt
                                                                       1260
 aaataataga atgaattcat tttagaattt aaatgatgct aataaaatag accattattc
                                                                       1320
 taaaagttta actaatttag aatcaaccct ggttgaaaat aaagccttaa gctgttttt
                                                                       1380
 tggaagactt taaatccttt atggctaaga gatgacagac agggccgagt gcggtggctc
                                                                       1440
                                                                       1500
 atgcctgtaa tcccagcact ttgggaggcc gaggcgggcg gatcacgagg tcaggaaatc
 aagaccatcc tggctaacac ggtgaaaccc tgtctctact aaaaaaataca aaaaaaatta
                                                                       1560
 gccgggcgtg gtggcgggcg cctgtagtcc cagctactca ggaggctgaa gcaggagcat
                                                                       1620
 ggtgtgaacc caggaggcag agcttgcagt gagctgagat cacaccactg cactccagcc
                                                                      1680
 1740
                                                                      1794
 <210> 80
 <211> 1280
 <212> DNA
 <213> Homo sapiens
 <400> 80
 ggcacgagta taaaggcccc tccacccagc ctctagccca tttctttctc tggcttttgc
 aggatteete atteteeetg aggtettaae tateaeatea tgeaegttet geeaetgetg
                                                                        60
 ttatcactgc tgctgctgct gctgctgctg tcagctagct ttgtgacttt cagcaccccc
                                                                       120
 acttccagca gaaattctag ctgccctgat tgtgagagtc tgaacaccgg tcttccatcc
                                                                       180
 ctgatgatgt ttggtggatc tctgctcaaa tgggttcaga acacacacgg ggtggaatca .
                                                                       240
ctcttgtcct ctgccaaggt gcgcctgctt ccaccagccc taggggttct gttcccaaga
                                                                       300
ctacaccctg gcactctgac ccttgtcttc cttttaattc ccttcctcac agtgtcttct
                                                                       360
tocacatoty acyttottag ctotttagag tocccaaaac tatotyttac catatttcat
                                                                       420
                                                                       480
tattgttaac tctaaagatt ttggcatcaa acaccctgca tttgaatgct agctgtgtca
                                                                       540
cacatcagat gctttacttt ggcaaatcat agaactttct gtcaataggg ataataatgg
tacctatatt gtaatattgt gagtgttact tggataataa agtacatagc acagtatttg
                                                                       600
gcacatagta attgctcaac aataccaatt gttattatta ttagactgtg ccctctaaat
                                                                      660
tatttgtcta cggattatga tctgtataaa tgacttatca attaagaaga ccacaggtat
                                                                      720
                                                                      780
gcagagtete ateaeteata caagaetgat gteaattaae taagagaagt ttegteaeta
accaggagtt tcacatcata gttccacact ttgcttctac tcccaatatg gcttgttgac
                                                                      840
ttttcactct ctttaccctg ttttctttct atggttccca gggctatcac ttttctttat
                                                                      900
tttggttaat acatataget gtacactgac ccagteteca tgaaaaatac tgtcatatac
                                                                      960
tecetettte ectettteee taatateate ateteataga gateaaacte acattteetg
                                                                     1020
gcaccattat tctttttata aaatacttta cttttaaatt tttacccaac tacgtctatg
                                                                     1080
ttattttagc tagctaagct gctataacaa agagatctaa atacagtggc ttaaatataa
                                                                     1140
cagaagcata tttttctctc atgtaacagc tagaggaatg tgtgtagtcc agagcataca
                                                                     1200
                                                                     1260
aaccacaagt cattcatgac
                                                                     1280
<210> 81
<211> 974
<212> DNA
<213> Homo sapiens
<400> 81
ggcacgagcc acaactacca gaactggagg gtgtacgacg tettggtget caaaggatee
                                                                      60
```

```
cagttatctg caagggctgc agatggatcc ccctgcaatg tcctcctgtg ctctgtggtc
  cccagcagac gcatggactc tgtgacctgg caggaaggga agggtcccgt gaggggccgt
                                                                    120
 gttcagtcct tctggggcag tgaggctgcc ctgctcttgg tgtgtcctgg ggaggggctt
                                                                    180
 tctgagccca ggagccgaag accaagaatc atccgttgcc tcatgactca caacaaaggg
                                                                    240
 gtcagtttta gcctggcagc ctccatcgat gcttctcctg ccctctgtgc ccttccacgg
                                                                    300
 ctgggacatg ccttggattc tgatgctgct gttcacaatg ggccagggag ttgtcatcct
                                                                    360
 ggccttcaga tcgtgtctgg aggcagaggt ccgtggggtt ccaggcagag gaaaccgaag
                                                                    420
 cggtgttaaa actgtggtgg aagccccagc agtttttgca aagaggccgt gaccacctgt
                                                                    480
 ggcgagggca gaccccagcc aggcctggaa cagatcaagc tacctggaaa ccccccagtg
                                                                    540
 accttgattc accaacatcc agcctgcgtc gcagcccatc attgcaatca agtggagaca
                                                                    600
 gagtcggtgg gagacgtgac ttatccagcc cacagggatg tacctgggag acctgtgcaa
                                                                    660
 cagegeegtg geaageeatg tggeeectge aggeattttg getgeageag etacegeeet
                                                                    720
 gacctgtttt ttgccaggac tgtggagcgg atagggggag taggagtaga gaagggaaca
                                                                    780
 agggagcaag ggaacaaggg acatttgaac atttaatgtg agaagacaaa catcctttgt
                                                                    840
 900
                                                                   960
 aaaaaaaaa aaaa
                                                                   974
 <210> 82
 <211> 1955
 <212> DNA
 <213> Homo sapiens
 <400> 82
 ggcagtgtcc ccaaggcacc gaaaccgagg cgggggtctc ggtccctccg cgcaaggagg
gaggeggacc gtacgtggca ggactcaccg ccccgcacgt ggcaggactc accgccccgc
                                                                    60
gccgtgttct ccgagccatg gcgccagcgc tgtggcgggc ctgcaacgga ctcatggccg
                                                                   120
cettettege getggeggee ttggtgcagg tggtgtacae aatecetgea gtactgacee
                                                                   180
tgcttgttgg acttaaccct gaagtcacag gtaatgttat ttggaaaagt atctctgcaa
                                                                   240
300
360
agcatggatt atcctgtgcc acagttcctc aaagaatcca gttggtggaa gaattcaatt
                                                                   420
ggctattgcc attgtaatca cactittccc atttatctca tgggtctaca tatatattaa
                                                                   480
caaggaaatg cggtcctctt ggccaactca ctgcaagaca gtaatttaaa taaattcaag
                                                                  540
aacttcgttt ttaaaatgaa tattttcaat caattttta taaacattag gggaacaagc
                                                                  600
caggaattta tttcaggtaa tttgggctaa tagttttaaa actccaaata actttttaag
                                                                  660
ggtgcatata attcgatgta agattggatg ggacaagtaa gaaatggtct gatattttcc
                                                                  720
agacactttc tgcagggtct tgtgtcataa tgtagtggaa aaggctagaa ataaagttta
                                                                  780
aaaatacagt totaacttaa otttgtacta tgttatttgg gcaatatata aacctcctgg
                                                                  840
tggatattat ctataaaata ggataatgcc agatctactt acttacacag taacaaggat
                                                                  900
caatctagat aatgtaagaa cactctgaag atataaagtg tttggaaaga ttacggaggg
                                                                  960
ctgcccatga ttaaaataga ggggagcagg gattggtaat atactgaaat agacattcaa
                                                                 1020
gagagggtat accccgatct ttttttttt ttttaagaca gtcccactct attgcccagg
                                                                 1080
ctggagtgca gtggcatgat catggctcac tgcagtcctg acctcccggg gctcaggtga
                                                                 1140
tectectace teagectece aagaagetac gactacaagt gtgcaccace atgceegget
                                                                 1200
aaatttttt aaattttttg tagaggcagg gtttcaccgt gttgtccagg ctggtcttga
                                                                 1260
```

attectgagt teaagegate tgtecacett ggeeteecaa agtgetggga ttacaggtgt

gagccaccat gcccagtcca gccctaaact aatcttatcc agagctggca tagtgcagtg

aactaaagga gaactctaga tgaatcaaat gagcaggcat gtcttggaaa gaaagggaag

ctggatagaa taaaggaatt agggaccaaa caagaaggca atagggacta taactacatt

ctaaatgaga aataaggtca aaatctatat acattcttta taaatggatg tccaaagtaa

tcctagggag gagagctttt ttttttcat ttccattttc atttaaaaat ggatacttga

ttattggaaa acttacaatt gtgtttggaa caacttgggt atttgaatct aattttccaa

ttgcaaattt tatgatacct aaatacagat aaagtatttc caatgaaaat ttagtgtcca

aatgagtggg gctataaatg taaaatacac tggattttaa agacatggta gaaaaagaac

agaaaatatt ttttgtattg attacatgtt gaaacaatat tttggctata atgggttaaa

tatactatta aagttgaaaa aaaaaaaaaa aaaaa

1320

1380

1440

1500

1560

1620

1680

1740

1800

1860

```
<210> 83
 <211> 638
 <212> DNA
 <213> Homo sapiens
 <400> 83
 ggcacgagag aggtcctggg gtaagagaaa aaaagtagtt atagcacttc gtccagcact
                                                                        60
 gacagcagcc gaacaaatgc tgaaaatctg actgtgtgac agaacgtatc actgatgact
                                                                       120
 gatagaaagc cctctttcac tctgattacc cactcactac atgaagtcct gaaaataaca
                                                                       180
 gagaaactgt tatatctttt taatgattta tttgcaagta ttgagatttg acctgaaaaa
                                                                       240
 caatgaaaca catgaacaca cttccgattt tctcctcgct gattagcttc ctgcctgctg
                                                                       300
 tragtgrigg argaagtgrt ataactactt tatgtaacat taragaacag ctagaggtrc
                                                                       360
 tggggtaaga gaaaaaagc acatcacaac aaatgtgaaa gccttcatta ttacacgttc
                                                                       420
cagtttgtct cgctgtgtag gcataagcta atggtttatt ttcagaaagc tgcctgaaac
                                                                       480
gttgctttgt attcttctag gaagaacttt aattcctcct gaggaactct actttctgag
                                                                       540
ccaaactgct aattttctgc ggaactgtct agaagatcat tcaagagacc ctgcagttgc
                                                                      600
actttctcgt aaaagttaaa aaaaaaaaa aaaaaaaa
                                                                      638
<210> 84
<211> 859
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (27)
<223> n equals a,t,g, or c
<400> 84
ccgggtcgac ccacgcgtcc ggcagangcg ggactgtcgt ctgggggagc cgcccaggag
                                                                       60
getectcagg cegaceceag accetggetg gecaggatga agtateteeg geaceggegg
                                                                      120
cccaatgcca ccctcattct ggccatcggc gctttcaccc tcctcctctt cagtctgcta
                                                                      180
gtgtcaccac ccacctgcaa ggtccaggag cagccaccgg cgatccccga ggccctggcc
                                                                      240
tggcccactc cacccacccg cccagecccg gccccgtgcc atgccaacac ctctatggtc
                                                                      300
acceacceyg acttegeeac geageegeag caegtteaga actteeteet gtacagacae
                                                                      360
tgccgccact ttcccctgct gcaggacgtg ccccctcta agtgcgcgca gccggtcttc
                                                                      420
ctgctgctgg tgatcaagtc ctcccctagc aactatgtgc gccgcgagct gctgcggcgc
                                                                      480
acgtggggcc gcgagcgcaa ggtacggggt ttgcagctgc gcctcctctt cctggtgggc
                                                                      540
acageeteea accegeacga ggeeegeaag gteaacegge tgetggaget ggaggeacag
                                                                      600
actcacggag acatcctgca gtgggacttc cacgactcct tcttcaacct cacgctcaag
                                                                      660
caggtgcgct ggactggggt cacctgatcg gggccacctg tccttcttgt ccaaattacc
                                                                      720
actccactcc agcctgggca acaaaagcga aaactccatc tccaaaaaaa taataataat
                                                                      780
840
aaaaaaaaa aaaaaaaaa
                                                                      859
<210> 85
<211> 1129
<212> DNA
<213> Homo sapiens
<400> 85
gctgcttccc aaggaccatg aaactcctgc tgctggctct tcctatgctt gtgctcctac
                                                                      60
cccaagtgat cccagcctat agtggtgaaa aaaaatgctg gaacagatca gggcactgca
                                                                     120
```

```
ggaaacaatg caaagatgga gaagcagtga aagatacatg caaaaatctt cgagcttgct
                                                                    180
gcattccatc caatgaagac cacaggcgag ttcctgcgac atctcccaca cccttgagtg
                                                                    240
actcaacacc aggaattatt gatgatattt taacagtaag gttcacgaca gactactttg
                                                                    300
aagtaagcag caagaaagat atggttgaag agtctgaggc gggaagggga actgagacct
                                                                    360
ctcttccaaa tgttcaccat agctcatgac ttcctctcgg ctatcactca cccctgtcct
                                                                    420
cagagtgata aactaagtca catacagata aagcactgaa aacaccacag tgaccctccc
                                                                    480
acccccacc aatatgtaat tctattaata gaaacagctg tgtaaagaag tctaaaattt
                                                                    540
tcactatttc caatgataaa ctcttcagtg ctcttcttga aatgtcacat tatttcccaa
                                                                    600
caagttatac ctatttttag tattcttgtt gctagtgcca tgcacaactt caatagctag
ttgctattcc aacaacaatt tcttcatgta tcgttctgtc ttctcaacag ctgtctttca
                                                                    660
                                                                    720
tggcagcata agtggtcatg atcaaaattc taaatcttgc atctgtgaga gtagctacta
                                                                    780
tgacactaaa agctttttt ctagaacagg agacacttca ggtgaagcat tcattctcct
                                                                    840
actaactatg gccttggagc caggttttat ctctcactgt aggaaattgg ccgcccagg
                                                                   900
tgtgagctat gaagactcct ttttgcccca gtggctttgg ggttgaaatg ctgtcgaaaa
                                                                   960
gcttttatgg ctctgtagac ccatcttttt gaccaagcct tgatcacaca tggacatcca
                                                                  1020
agggtaatca tggaccccca attgtgggtg aaaggatgga tcatttatct acctgattac
                                                                  1080
1129
```

```
<210> 86
 <211> 2674
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (2607)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (2611)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (2621)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (2634)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (2650)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (2660)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (2669)
```

WO 99/31117 PCT/US98/27059 46

<223> n equals a,t,g, or c

```
<400> 86
gatecetece ateteacagt accteacagg tetetteece egageagtge attgetggag
                                                                         60
cgaggagaag ctcacgaatc agctgcaggt ctctgttttg aaaaagcaga gatacagagg
                                                                        120
cagaggaaaa gggtggactc ctatgtgacc tgttcttaga gcaagacaat caccatctga
                                                                        180
attccagaag ccctgttcat ggttggggat attttctcga ctgcatggaa tcagaaagaa
                                                                        240
gcaaaaggat gggaaatgcc tgcattcccc tgaaaagaat tgcttatttc ctatgtctct
                                                                        300
tatctgcgct tttgctgact gaggggaaga aaccagcgaa gccaaaatgc cctgccgtgt
                                                                        360
gtacttgtac caaagataat gctttatgtg agaatgccag atccattcca cgcaccgttc
                                                                        420
ctcctgatgt tatctcatta tcctttgtga gatctggttt tactgaaatc tcagaaggga
                                                                        480
gttttttatt cacgccatcg ctgcagctct tgttattcac atcgaactcc tttgatgtga
                                                                       540
tcagtgatga tgcttttatt ggtcttccac atctagagta tttattcata gaaaacaaca
                                                                       600
acatcaagtc aatttcaaga catactttcc ggggactaaa gkcattaatt cacttgagcc
                                                                       660
ttgcaaacaa caatctccag acactcccaa aagatatttt caaaggcctg gattctttaa
                                                                       720
caaatgtgga cctgaggggt aattcattta attgtgactg taaactgaaa tggctagtgg
                                                                       780
aatggcttgg scacaccaat gcaactgttg aagacatcta ctgcgaaggc cccccagaat
                                                                       840
acaagaagcg caaaatcaat agtctctcct cgaaggattt cgattgcatc attacagaat
                                                                       900
ttgcaaagtc tcaagacctg ccttatcaat cattgtccat agacactttt tcttatttga
                                                                       960
atgatgagta tgtagtcatc gctcagcctt ttactggaaa atgcattttc cttgaatggg
                                                                      1020
accatgtgga aaagaccttc cggaattatg acaacattac aggcacatcc actgtagtat
                                                                      1080
gcaagcctat agtcattgaa actcagctct atgttattgt ggcccagctg tttggtggct
                                                                      1140
ctcacatcta taagcgagac agttttgcaa ataaattcat aaaaatccag gatattgaaa
                                                                      1200
ttctcaaaat ccgaaaaccc aatgacattg aaacattcaa gattgaaaac aactggtact
                                                                      1260
ttgttgttgc tgacagttca aaagctggtt ttactaccat ttacaaatgg aacggaaacg
                                                                      1320
gattctactc ccatcaatcc ttacacgcgt ggtacaggga cactgatgtg gaatatctag
                                                                      1380
aaatagtcag aacacctcag acactcagaa cgcctcattt aattctgtct agtagttccc
                                                                      1440
ascgtcctgt aatttatcag tggaacaaag caacacaatt attcactaac caaactgaca
                                                                      1500
ttcctaacat ggaggatgtg tacgcagtga agcacttctc agtgaaaggg gacgtgtaca
                                                                      1560
tttgcttgac aagattcatt ggtgattcca aagtcatgaa atggggaggc tcctcgttcc
                                                                      1620
aggatattca gaggatgcca tcgcgaggat ccatggtgtt ccagcctctt caaataaata
                                                                      1680
attaccaata tgcaattett ggaagtgatt acteetttae teaagtgtat aactgggatg
                                                                      1740
cagagaaagc caaatttgtg aaatttcagg aattaaatgt tcaggcacca agatcattca
                                                                      1800
cacatgtgtc cattaataag cgtaattttc tttttgcttc cagttttaag ggaaatacac
                                                                      1860
agatttacaa acatgtcata gttgacttaa gcgcatgaga caccaaattc tgtggctgcc
                                                                      1920
atcagaaatt ttctacagta catgacccgg atgaactcaa tgcatgatga ctcttcttat
                                                                      1980
cacacttgca aatgaatgcc tttcaaacat tgagactgct agaaccaagc actaccagta
                                                                      2040
tctccatcct taactgtcca gtccagtgat gtgggaagtt accttttata agacaaaatt
                                                                      2100
taattgtgta actgttcttt gcagtgaaga tgtgtaaata agcgtttaat ggtatctgtt
                                                                      2160
actccaaaaa gaaatattaa tatgtacttt tccatttatt tattcatgtg tacagaaaca
                                                                      2220
actgccaaat aaaatgttta cattttcttt cataaaaaaa aaaaaaaaa aactcgaggg
                                                                      2280
ggggcccggt acccaattcg ccctatagtg agtcgtatta caattcactg gccgtcgttt
                                                                      2340
tacaacgtcg tgactgggaa aaccctggcg ttacccaact taatcgcctt gcagcacatc
                                                                      2400
cccctttcgc cagctggcgt aatagcgaag aggccgcacc gatcgccctt cccaacagtt
                                                                      2460
gcgcagcctg aatggcgaat ggcaaattgt aagcgttaat attttgttaa aattccgcgt
                                                                      2520
taaattttgt taaatcagct cattttttaa cccaataggc cgaaattcgg caaaaatccc
                                                                      2580
ttattaatca aaagaaatag aaccganaat nggggttgaa ntgttgtttc caantttggg
                                                                      2640
aaacaaaaan tcccacttan tttaaaagna aacg
                                                                      2674
```

<210> 87

<211> 1636 <212> DNA

<213> Homo sapiens

<220>

<221> SITE

```
<222> (1624)
 <223> n equals a,t,g, or c
  <400> 87
 togacccacg cgtccggctg agtgtgagct gagcctgccc caccaccaag atgatcctga
                                                                           60
 gcttgctgtt cagccttggg ggccccctgg gctgggggct gctgggggca tgggcccagg
                                                                         120
 cttccagtac tagcctctct gatctgcaga gctccaggac acctggggtc tggaaggcag
                                                                         180
 aggetgagga caccagcaag gaccccgttg gacgtaactg gtgcccctac ccaatgtcca
                                                                         240
 agctggtcac cttactagct ctttgcaaaa cagagaaatt cctcatccac tcgcagcagc
                                                                         300
 cgtgtccgca gggagctcca gactgccaga aagtcaaagt catgtaccgc atggcccaca
                                                                         360
 agccagtgta ccaggtcaag cagaaggtgc tgacctcttt ggcctggagg tgctgccctg
                                                                         420
 gctacacggg ccccaactgc gagcaccacg attccatggc aatccctgag cctgcagatc
                                                                         480
 ctggtgacag ccaccaggaa cctcaggatg gaccagtcag cttcaaacct ggccaccttg
                                                                         540
 ctgcagtgat caatgaggtt gaggtgcaac aggaacagca ggaacatctg ctgggagatc
                                                                         600
 tccagaatga tgtgcaccgg gtggcagaca gcctgccagg cctgtggaaa gccctgcctg
                                                                         660
 gtaacctcac agctgcagtg atggaagcaa atcaaacagg gcacgaattc cctgatagat
                                                                         720
 cettggagea ggtgetgeta ceccaegtgg acaeetteet acaagtgeat tteageeeca
                                                                         780
 tctggaggag ctttaaccaa agcctgcaca gccttaccca ggccataaga aacctgtctc
                                                                         840
 ttgacgtgga ggccaaccgc caggccatct ccagagtcca ggacagtgcc gtggccaggg
                                                                         900
 ctgacttcca ggagcttggt gccaaatttg aggccaaggt ccaggagaac actcagagag
                                                                         960
 tgggtcagct gcgacaggac gtggaggaac gcctgcacgc ccagcacttt accctgcacc
                                                                        1020
 gctcgatctc agagctccaa gccgatgtgg acaccaaatt gaagaggctg cacaaggctc
                                                                        1080
 akgaggcccc agggaccaat ggcagtctgg tgttggcaac gcctggggct ggggcaaggc
                                                                        1140
 ctgagccgga cagcctgcag gccaggctgg gccagctgca gaggaacctc tcagagctgc
                                                                        1200
 acatgaccac ggcccgcagg gaggaggagt tgcagtacac cctggaggac atgagggcca
                                                                        1260
 ccctgacccg gcacgtggat gagatcaagg aactgymctc cgaatcggac gagactttcg
                                                                        1320
 atcagattag caagktgkwg cggcaggtgg aggagctgca ggtgaaccac acggcgctcc
                                                                       1380
 gtgagctgcg cgtgatcctg atggagaagt ctctgatcat ggaggagaac aaggaggagg
                                                                       1440
 tggagcggca gctcctggag ctcaacctca cgctgcagca cctgcagggt ggcatgccga
                                                                       1500
cctcatcaag tacgtgaagg actgcaattg ccagaagctc tatttagacc tggacgtcat
                                                                       1560
 ccgggagggc agagggacgc cacgcgtgcc ctggaggaga cccaggtgag cctggacgar
                                                                       1620
cggnggcaag ctggac
                                                                       1636
<210> 88
<211> 1639
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (12)
<223> n equals a,t,g, or c
<400> 88
gtgacactat anaagtacgc ctggcagggt accggtccgg caattcgcgg ccgcgtcgac
                                                                         60
gtcaggcggg ccgtgggttc ccggaggggs tcttgaggcg ccatttcaag tcgccccag
                                                                        120
cctctcccac agcactcctg ttttcccggg cctcatcatg gcccacggcc ctcagtcgct
                                                                        180
gtggagcctg ggcttcacag tgacactcac gtttgaactc ccggtcggct gtgtgcttgg
                                                                        240
tagaatttgt catccaatac aggcgtgtaa cacgggcttg atgacaccca ccccacaggg
                                                                        300
cccctgcagg accgagatga tgtccaatga caagccctgg cttccagcca atgctcctgc
                                                                        360
ccacatetet eteccaggag ccaggettae etetacetgt gcacetggge tgtgacteat
                                                                        420
gactggaatg atctggctgg gcctgttccc ccaccagact tattttcagg cgccccagca
                                                                        480
gccaccaaac atctgtcaac tgaagtaatg aacctgcagt tgagaggcag ctaaacctag
                                                                       540
gttgaaggtt agggagacag ctgagttgag gtcaaatccc cccggccagt tagcctttct
                                                                       600
gagcctattt cctcaattgt aaaaggaaga caatcatgat gctgacctca gaatcsagcg
                                                                       660
aggaggaagt gaggaggtgc atgtgaagca ttgtgcgtga ctggtggggc taactgggct
                                                                       720
```

780

ctggaagcgg tarctctggg gccctaaccc ctttctgcct catgctaatt gacctatggc

```
atgtccagtg acatcatgac tgaaaaaatg atttgaaart ataatcgctg tcaggaattg
                                                                         840
 tetectggte teaaacteet aggettaagg aatttgeeca eettageeta eeaaagggeg
                                                                         900
gggcttacaa gcatgarcca tggcacccgg ccccaaagtg ttttttctat tctctcagtc
                                                                         960
macagttaca cagaaaattt ctgtgaccac tggtcacgaa agggagtgga ggtctctccc
                                                                        1020
taccggcaac caagcagtcg attctgcagt ggacaccagc tgggtgttct cttattgaat
                                                                        1080
taattctgac actatctgtc cagagatagc attagattcc acaggttgag gacttagtcc
                                                                        1140
ccacttgtcc cttatttctg atgctgatca caagamctar gttattttgc cggtgattct
                                                                        1200
gactgactgg ctattaatta gggtttctgt gacccactcc ttgggttcaa ttaatttgct
                                                                        1260
agagaactcc ctcatggaat tcagagaaac acatttacca gcttattata aaggctgcta
                                                                        1320
caaaggatac agatgagatg cgcagagcaa cgtgtgggat ggagtgcaga gcttccgcgc
                                                                       1380
cctctcctgg agcaccactc ttcaggaacc tccatgtgtt cagctattca gaagctccct
                                                                       1440
ggacccagtc ctttcgggtt tttatggaag cttcattatg tagacatgat taattatacc
                                                                       1500
attggtcatt ggtgatcaac ttaaccttca gcccttctcc cctcccggag gttggagggt
                                                                       1560
ggggctgaaa cattccaact tacaggcccg tcgacgcggc cgcgaattcc cgggtcgacg
                                                                       1620
agctcactag tcggcggcc
                                                                       1639
<210> 89
<211> 1860
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (1846)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (1848)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (1853)
<223> n equals a,t,g, or c
<400> 89
ctcaccagms ggaaagtacg agtcggctca gcctggaggg acccaaccag agcctggcct
                                                                         60
gggagccagk atggccatcc acaaagcctt ggtgatgtgc ctgggactgc ctctyttcct
                                                                        120
gttcccaggg gcctgggccc agggccatgt cccacccggc tgcagccaag gcctcaaccc
                                                                        180
cctgtactac aacctgtgtg accgctctgg ggcgtggggc atcgtcctgg aggccgtggc
                                                                        240
tggggcgggc attgtcacca cgtttgtgct caccatcatc ctggtggcca gcctcccctt
                                                                        300
tgtgcaggac accaagaaac ggagcctgct ggggacccag gtattcttcc ttctggggac
                                                                        360
cetgggeete ttetgeeteg tgtttgeetg tgtggtgaag eeegaettet eeacetgtge
                                                                        420
ctctcggcgc ttcctctttg gggttctgtt cgccatctgc ttctcttgtc tggcggctca
                                                                       480
cgtctttgcc ctcaacttcc tggcccggaa gaaccacggg ccccggggct gggtgatctt
                                                                       540
cactgtggct ctgctgctga ccctggtaga ggtcatcatc aatacagagt ggctgatcat
                                                                       600
caccctggtt cggggcagtg gcgagggcgg ccctcagggc aacagcagcg caggctgggc
                                                                       660
cgtggcctcc ccctgtgcca tcgccaacat ggactttgtc atggcactca tctacgtcat
                                                                       720
gctgctgctg ctgggtgcct tcctgggggc ctggcccgcc ctgtgtggcc gctacaagcg
                                                                       780
ctggcgtaag catggggtct ttgtgctcct caccacagcc acctccgttg ccatatgggt
                                                                       840
ggtgtggatc gtcatgtata cttacggcaa caagcagcac aacagtccca cctgggatga
                                                                       900
ccccacgctg gccatcgccc tcgccgccaa tgcctgggcc ttcgtcctct tctacgtcat
                                                                       960
ccccgaggtc tcccaggtga ccaagtccag cccagagcaa agctaccagg gggacatgta
                                                                      1020
ccccacccgg ggcgtgggct atgagaccat cctgaaagag cagaagggtc agagcatgtt
                                                                      1080
```

```
cgtggagaac aaggcctttt ccatggatga gccggttgca gctaagaggc cggtgtcacc
                                                                        1140
 atacagcggg tacaatgggc agetgctgac cagtgtgtac cagcccactg agatggccct
                                                                        1200
 gatgcacaaa gttccgtccg aagagcttac gacatcatcc tcccacgggc caccgccaac
                                                                        1260
 agccaggtga tgggcagtgc caactcgacc ctgcgggctg aagacatgta ctcggcccag
                                                                        1320
 agccaccagg cggccacacc gccgaaagac ggcaagaact ctcaggtctt tagaaacccc
                                                                        1380
 tacgtgtggg actgagtcag cggtggcgag gagaggcggt cggatttggg gagggccctg
                                                                        1440
 aggacctggc cccgggcaag ggactctcca ggctcctcct cccctggca ggcccagcaa
                                                                        1500
 catgtgcccc agatgtggaa gggcctccct ctctgccagt gtttgggtgg gtgtcatggg
                                                                        1560
 tgtccccacc cactcctcag tgtttgtgga gtcgaggagc caaccccagc ctcctgccag
                                                                        1620
 gatcacctcg gcggtcacac tccagccaaa tagtgttctc ggggtggtgg ctgggcagcg
                                                                        1680
 cctatgtttc tctggagatt cctgcaacct caagagactt cccaggcgct caggcctgga
                                                                        1740
 tettgeteet etgtgaggaa caagggtgee taataaatae atttetgett tattaaaaaa
                                                                        1800
 aaaaaaaaaa aaaaaaactc gagggggggc ccgtacccaa tcgccngnga tgntagtata
                                                                        1860
 <210> 90
 <211> 839
 <212> DNA
 <213> Homo sapiens
<400> 90
ggcacgaggg ctacgatect acagtggaga atagatgagt acagcattet gecetattea
                                                                         60
ttcatcattg gggtccatgg ttatgtgctt gtgtattctg tcacctctct gcatagcttc
                                                                        120
caagtcattg agagtctgta ccaaaagcta catggaaggc catgggaaaa cccgggtgcc
                                                                        180
agtggttcta gtggggaaca aggcagatct ctctccagag agagaggtac aggcagttga
                                                                        240
aggaaagaag ctggcagagt cctggggtgc gacatttatg gagtcatctg ctcgagagaa
                                                                        300
tcagctgact caaggcatct tcaccaaagt catccaggag attgcccgtg tgggagaatt
                                                                        360
cctatgggca agagegtege tgccatetea tgtgageeet tgggtgtggg gtaactgeet
                                                                        420
tgcttctgcc cccggcactt gccatgttcc agtggggggc agatcctcag gacttcacgg
                                                                        480
gtatggttgc cagctgtgtt cctggcccct ggacacacag tgtggcatcc tcatgtttgc
                                                                        540
acactttccc caggetecag tggeetggat gteaatgttt acaaagggge aaggaeetet
                                                                        600
catggacact ggcctctagc cctctgtttt tgtttgatga attctgttat aacctatggg
                                                                        660
gtcaggatat gagtcctggg cattatttat ccaggaccca tcctcttggg tgggttttgg
                                                                        720
gtgttggctg ggtaagggga gccggggact tctgaaatag agctggctcc ctggggtgac
                                                                        780
aatgtatata tgcaaataaa ttgagaaatc ttttgttgtt gaaaaaaaaa aaaaaaaaa
                                                                        839
<210> 91
<211> 1145
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (386)
<223> n equals a,t,g, or c
<400> 91
aattcggcac gaggacatat tggccattta ctctactaat aaaagagtac tatctactca
                                                                         60
gtgtcattta ctgttactgt agtaattaat gcctttggaa gaatcttttg aaatagttct
                                                                        120
caaattggta ccactacttg gtttggaatt atttttttt cttttcataa tcaatggtta
                                                                       180
tataaatgta tattgtccta gtcagtattt tatatatgct aaggactcac tagctggctt
                                                                       240
ggcactaata cctcaataaa aggaatactt cttttggaat catgaaacaa aagtgartaa
                                                                       300
acctccaagt tatttttcca accaaccttc tttgaaaaat cttggatgag tcactcaaat
                                                                       360
caagacatgt tataaaatta tctgtnattt tggtagaaca tatacattgt yctaataata
                                                                       420
atttycaaat attcagtgka acygtaagka tgagaataca ggttgaatat cycttatcca
                                                                       480
aaatgcttgg gaccagaagt cttttggatt ycaaattttt aaatatttac atcatactta
                                                                       540
```

```
ccagtttaac atccctaatt caaaaattca aaattcagaa tgctccaata atcgtttcct
                                                                         600
 ttgascatca tgtcagtgct caaaaagttg cagattttga ggtatttcag atttttgaat
                                                                         660
 taggaagact caacttgtac tatcattcta tagactttat gattgggtag actacatgag
                                                                         720
 tattgaaccc agaaatcatt gtctagcaaa agccagtata gtgattaatt accctgtgac
                                                                         780
 tattatataa tgttcaaaaa agctaacata ttagaatgtc cttagcgtgc agagagcaaa
                                                                         840
 cagagacaaa aagaaaagtt accctgaaaa gtttgtcaga aaaatagaat atcagacgct
                                                                         900
 raactactca tccagaattt tgtcraaaaa gaaaaataag ataaaattca ctggtagaca
                                                                         960
 aaaagtagta acataccagt ttgtaatttc tcagtttcaa accatgaata tgtatttgta
                                                                        1020
 taccaaaaat catttcagga gtcagagaag gaggatatgc cttttatgtg gagactttaa
                                                                        1080
 acataaaatt ggaaaaaaaa aaaaaaaaaa actcgtaggg ggggtcccgt acccaatcgt
                                                                        1140
 cctgt
                                                                        1145
 <210> 92
 <211> 2050
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (515)
 <223> n equals a,t,g, or c
 <400> 92
aagaatggca taaattcatc cagcttctta cagaattcca aatgcggaat gtagatttt
                                                                         60
tatatagtaa tottgagttt attotaccat taccagttga taccattcca gaaactaaaa
                                                                        120
acttttgtgg cccatcagta actgtggatg ccagtgcagc aacaaaaagt atgaattgtc
                                                                        180
ttgctaggaa acactctgaa agagaacagc cattgaaaaa gtcccagaaa aagaaacaaa
                                                                        240
agaaaacatt ggtaatatta gatgatagtg atctatttga cactgacttg gactttcctg
                                                                        300
atcaatctat tagcctgtcc tctgtatcat cttcctcaaa tgcagaagaa agcaaaaccg
                                                                        360
gagacgaaga aagcaaagcc agagacaaag gaaacaatcc agagacaaag aaatctattc
                                                                        420
cttgtcctcc taaaacaact ggcaggaaaa aaatgttctg ccctgtttct cattgtttaa
                                                                        480
attetetete tgagtteatg ggataacatg teetnettag atgeaetttt aactgatgta
                                                                        540
agggracaaa acaaatacgg tagaaatgac tttagttgga caaatggaaa ggttacaagt
                                                                        600
ggactttgtg atgagtttag tettgagagt aatgatggat ggaettetea aagetetgga
                                                                        660
gaattaaagg cagctgcaga agctctcagc tttactaaat gttcttctgc tatttcaaaa .
                                                                        720
gcatkggaaa ccttgaattc ttgcaagaaa ttaggaagag atccaaccaa cgatcttact
                                                                        780
ttttatgttt cacaaaagcg caataatgta tactttagtc agtcagcagc taatttagac
                                                                        840
aatgcttgga agaggatatc agtcattaaa agtgtatttt cgagtcgatc tcttctctat
                                                                        900
gtgggtaata gacaagctag tataattgaa tacctgccaa cccttcgaaa catctgtaag
                                                                        960
actgagaagc taaaagaaca aggaaaaagt aaaagaagat tcctgcacta ttttgaagga
                                                                       1020
attcatcttg acattccaaa agagactgtg aatactttgg cagctgactt cccttaatgt
                                                                      1080
tccatactaa caatgctttg tatagattat catgtggtcc ttaagataca tttttatatt
                                                                      1140
atgtggatct tcatggaaaa gtatatttct cgatgtacat tttaaacaaa caatttgtat
                                                                      1200
attttttat tggcgggtaa atatttaaaa tatttgagtt acaaatttta tatatgattg
                                                                      1260
taattttttt tctgaatttt ttgtattatc tgatttagct ttgttggagt attttttgta
                                                                      1320
tgtgagtgaa ctgtttctgg aaggtaragt tcattaagat gaactcccta tttcaagtgt
                                                                      1380
ttatattata tattagetta atatteagat acattatett ggetgetaae attagtgtea
                                                                      1440
ctaaagttgg tatacaatct cccactgcta aatttgactg gctttacaaa aacaaaaaca
                                                                      1500
ttatctggtg aattatattt ttaacctaaa agttaaggat cctcatattg tacagttttt
                                                                      1560
tttgtgtgct ttttttttt tttttgagac ggaatcttgc tctgtcaccc aggctggagt
                                                                      1620
gcagtggcct ggtatcggct cagtgcaact tttgcctccc gggttcaagc gattatcctg
                                                                      1680
cctcagcctc ctgaatagck gggattacag gcatgtgcca ccttgcccag ctaatttttg
                                                                      1740
tatttttaga agagacaggg ttttaccatg ttggttaggc tggtctctta actcckgacc
                                                                      1800
tcaagtgatc catctgcctc ggcctcccaa agtgctggga tcacaggcgt gagccacctc
                                                                      1860
acctggccta tattgtacag ttttgaacag tatagatgca tacctgttta caaatgtgta
                                                                      1920
tgaagataga tatttttacc tcttatttgt tcaatttact ttktcttgta ttaattagta
                                                                      1980
```

tattgatga artagaggab	
tattgateta attaaaggtt aaagetaaag getttatgaa atgtttaaaa aaaaaaaaaa	2040
**************************************	2050
<210> 93	
<211> 1173	
<212> DNA	
<213> Homo sapiens	
<400> 93	
tcgacccacg cgtccgaaac aaaggaaaat atccccaaag ttgttttcta gatttgtggc	
	60
	120
	180
	240
	300
	360
	420
	480
	540
	600
	660
	720 780
	840
	900
	960
cagcotgggc tatatagcaa gaccocatca ctacaaattt tttacaaatt agctaggtgt	1020
	1080
	1140
gagogagaco oggiotocaa aaaaaaaaaa aaa	1173
<210> 94	
<211> 822	
<212> DNA	
<213> Homo sapiens	
<400> 94	
ggcacgaggt tecetetece cagagecate ggccaggtae caaageteag etgtatggat	
	60
gggctgtgtt ctgtgataac tggagggtgc attctttc tgcactggag gaagaacttg	120
	180
	240
	300
	360
	420 480
tececatice caetteceat ettteaggag gtgeeetttg eeceaeeett gtgeaaceta	480 540
	600
	660
	720
	780
catgctatga aacatttgaa gcaaaaaaaaa aaaaaaaaaa	822
	-22
<210> 95	

<210> 95

<211> 1077

<212> DNA

<213> Homo sapiens

<400> 95

```
ggcacgagtt ggtgggcaat agcgcttttc tctcaagggg cttttggcta tgtgctgccc
atcatttcat tcatccttgc ctggattgag acgtggttcc tggatttcaa agtgttacct
                                                                         60
caagaagcag aagaagaaaa cagactcctg atagttcagg atgcttcaga gagggcagca
                                                                        120
cttatacctg gtggtctttc tgatggtcag ttttattccc ctcctgaatc cgaagcagga
                                                                        180
tctgaagaag ctgaagaaaa acaggacagt gagaaaccac ttttagaact atgagtacta
                                                                        240
cttttgttaa atgtgaaaaa ccctcacaga aagtcatcga ggcaaaaaga ggcaggcagt
                                                                        300
ggagtetece tgtegacagt aaagttgaaa tggtgaegte caetgetgge tttattgaac
                                                                        360
agctaataaa gatttattta ttgtaatacc tcacagacgt tgtaccatat ccatgcacat
                                                                        420
ttagttgcct gcctgtggct ggtaaggtaa tgtcatgatt catcctctct tcagtgagac
                                                                        480
tgagcctgat gtgttaacaa ataggtgaag aaagtcttgt gctgtattcc taatcaaaag
                                                                        540
acttaatata ttgaagtaac acttttttag taagcaagat acctttttat ttcaattcac
                                                                        600
agaatggaat ttttttgttt catgtctcag atttattttg tatttctttt ttaacactct
                                                                       660
acatttccct tgttttttaa ctcatgcaca tgtgctcttt gtacagtttt aaaaagtgta
                                                                       720
ataaaatctg acatgtcaat gtggctagtt ttatttttct tgttttgcat tatgtgtatg
                                                                       780
gcctgaagtg ttggacttgc aaaaggggaa gaaaggaatt gcgaatacat gtaaaatgtc
                                                                       840
accagacatt tgtattattt ttatcatgaa atcatgtttt tctctgattg ttctgaaatg
                                                                       900
ttctaaatac tcttattttg aatgccaaaa tgacttaaac cattcatatc atgtttcctt
                                                                       960
tgcgttcagc caatttcaat taaaatgaac taaattaaaa aaaaaaaaa aaaaaaa
                                                                      1020
                                                                      1077
```

```
<210> 96 <211> 2092
```

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (637)

<223> n equals a,t,g, or c

<400> 96

```
gaatteggea yggegaeett tgtgagegag etggaggegg ecaagaagaa ettaagegag
 gccctggggg acaacgtgaa acaatactgg gctaacctaa agctgtggtt caagcagaag
                                                                          60
 atcagcaaag aggagtttga ccttgaagct catagacttc tcacacagga taatgtccat
                                                                        120
 teteacaatg attteetet ggeeattete acgegttgte agattttggt ttetacacea
                                                                        180
gatggtgctg gatctttgcc ttggccaggg ggttccgcag caaaacctgg gaaaacccaa
                                                                        240
gggaaagaaa aagctttctt ctgttcgtca gaaatttgat catagattcc agcctcaaaa
                                                                        300
tectetetea ggageecage aatttgtgge aaaggateee caagatgatg acgaettgaa
                                                                        360
actitigatice cacacaatga tgcttcccac tcgaggccag cttgaaggga gaatgatagt
                                                                        420
gactgcttat gagcatgggc tggacaatgt caccgaggag gctgtttcag ctgttgtcta
                                                                        480
tgctgtggag aatcacctta aagatatact gacgtcagtt gtgtcaagaa ggaaagctta
                                                                        540
teggttacga gatggtcatt ttaaatatge etttggnagt aacgtgacce egeagecata
                                                                        600
cctgaagaat agtgtagtag cttacaacaa cttaatagaa agccctccag cttttactgc
                                                                        660
tecetgtget ggtcagaate cagettetea eccaececet gatgatgetg ageageagge
                                                                        720
tgcactcctg ctggcatgct ccggagacac tctacctgca tctttgcctc cggtgaacat
                                                                        780
gtacgatctt tttgaagctt tgcaggtgca cagggaagtc atccctacac atactgtcta
                                                                        840
tgctcttaac attgaaagga tcatcacgaa actctggcat ccaaatcatg aagagctgca
                                                                        900
gcaagacaaa gttcaccgcc agcgcttggc agccaaggag gggcttttgc tgtgctaaat
                                                                        960
taggatttga gggtgtggga ccctcaccra attcattgat tactgaaaat tgaatgtttt
                                                                       1020
ttgggtccac atttcaaggc tgaagtgtgt agtgtatata taacctttcc tatggaaatg
                                                                      1080
tgacattgag tacattttgt gttgctgttg tgaagccatt aatataaatc tttggtaatg
                                                                      1140
acccatatct ctatatgtat gtgttcccag ttgtgggagc aggcactaat gaaatcctgt
                                                                      1200
gcctggaatg gagatattta ggtacctgag gcttagtgtc ctgtggtctg catgtaagat
                                                                      1260
agatgacatc ctagaacaaa gaagctgttt taacttaatc cccctgatca gcaggatatc
                                                                      1320
                                                                      1380
```

53	
tgtgtgttca gtgacatcat acattetgta tetagaagte taaaatttet geetttetee	2.4.0
	1440
and a succession and the succession of the succe	1500
taggaatat gattiggaag tottetatat actagacasa ataana	1560
The state of the s	1620
gtttaattat tootatagaa harrana tgcccaaaaa ctttgattgg cagtttette	1680
ggttaattat tectatagaa tgtattttaa gaaatetata caaattggat atatgettgg	1740
taattotooa gittotagga ggtacotatt tota	1800
taatteteea gtttetagga ggtacetatt tetacegttt caagtgatga agtgaaaata	1860
atttacattc gatagtgtta ctgataacaa acctacttaa gagatatgtt gctttttact	1920
taagggatag tgttgataga taaattagaa tgtatagata ggtttgtgaa agtctaaata	1980
magadaged designation and designation of the state of the	2040
ctttaaatgt gacaaataaa ccttttggga gaaaaaaaaa aaaaaaaaac tc	2092
<210> 97 <211> 1352 <212> DNA <213> Homo sapiens <400> 97 ggcacgaggt gatccaccca cgttggcctc ccaaagtyct gggattacag gtgtgagccg	
Ctgccctag ccctagatag atttpcctt ccdadgtgct gggattacag gtgtgagccg	60
ctgccctgg ccctaaatag attttaaata agttttctgg atgcacacac tagtaaacac	120
	180
agectedata ttttcatett caaaatcaaa anna	240
and the same of th	300
gandada acattadal Cttttttttttttttttttttttaagagg ganna	360
sadagagaga gacacogco caadaaaaaa aaaaaaaaaa aaaaaaaaa	420
and substitution of the su	480
and a second sec	
and the state of t	540
by a decade of geographic transfer of the contract of the cont	600
sugardad detections that the standard deachters about the	660
-yyouddou ddadyyddii acacacaggg gataagaaaa taatggaast aantal	720
and the deady act and the second action of the second action and the second action actions are second actions as a second action action actions are second actions as a second action act	780
and the same of th	840
	900
agaaggttta cctgtacccc tcaaataact atcaccagaa tgaaggcagc agttacatga	960
agaaycacaa agaaccacca ctaaagatct aatggtaccc aatccctttt aaagtatgtc	1020
tgtgtctata ttggttaacc ttttcttatc tgaaatacaa atgccacatg atctcactta	1080
taagtggaag ctaaacattg agtacagatg gacacacaca aaaagaacaa cagacacagg	1140
ggtttacttg agagagaagg gtgggggagg gaaaagatac ctattgggta	1200
ctatgctcac tacctgggtg atgaatcat the suggets gaaaagatac ctattgggta	1260
ctatgctcac tacctgggtg atgaaatcat ttgtacacca aactccagtg acacacaatt tacttatgta gcaaacctgc acaaaacaac cc	1320
A Sam Sammer acquaged CC	1352
<210> 98 <211> 913 <212> DNA <213> Homo sapiens	·
<400> 98	
ggcacgagtg aatattttta aggctcttga tttgctggag gactgaaaaa aatgaagtga	60
sister garacted trydeliate fritagages togethoogh there	120
o s s s s s s s s s s s s s s s s s s s	180
sales aggregagy didadidida cottactatt tagatagos the	240
and a second sec	300
agttcctgtg agcctgaggt gctgcatgtg cccacccccg tgtacaggcc ctgccccagc	360
	300

```
cacageeeae teacettttg acceteetge tetgeetata cagtttgaat accageagge
  tcagctggag gctgagatcg aaaacctctc atggaaagtg gagcgtgcag acagctatga
                                                                        420
  cagaggggac ttggagaacc agatgcatat ageggageag eggaggagaa ecetgetgaa
                                                                        480
  agatttccat gacacctaag ttgggatgtg gatgtgccgg ggtgaggaag atgtggctgc
                                                                        540
  aaggtctccc ggctgccata ctgcatgctg caggctctgc ctttcatgac cccaggcaac
                                                                        600
  agccagggcc ccactcctga gagacactgg caacacctct tagttgattt ctgttttctt
                                                                        660
  ctcttttcac tttttgtttc taccagggta gaggccatgt tgaactggcc tcttttcagg
                                                                        720
  acttttattt ccccctggat ggttgttggg agggagggaa agtgttttct gaatggctat
                                                                        780
  taatagtatt agatcattac aacttatgta actttcaaag gttgtacaat tatacaaaaa
                                                                        840
                                                                        900
  aaaaaaaaa aaa
                                                                        913
 <210> 99
 <211> 721
 <212> DNA
 <213> Homo sapiens
 <400> 99
 ggcacgagct taaatacact tttatttgct atttctgtga agcaaactgc cgttggactt
 cccattaaac aatgtctaga atctttgcca ttgtctctct atgctagtca cacttacagc
                                                                        60
 acctactttc agactcctca tctttcaacc tgttgtctcc tttcagttgc tggattaagt
                                                                       120
 atcatttggg ctacatgttc cccccttgtc cctaaaattc cttcccattc caccccagct
                                                                       180
 attctaatgc atttaataat atgtctttgg atatgtatga tttcttcaat gtacagtgga
                                                                       240
 atgtattcca atttacataa atagttctac gttattttct gttatggccc ttcaatcaat
                                                                       300
 tccaagtttc accttattga tctcattctt tctttccact cagtgcttaa gatgtgtgta
                                                                       360
 caactatgaa tgcatcctat tcatggcatt taactgcagg atggtgttct agtattcatc
                                                                       420
 cgaatttccc ttatctgatc cactagtgat ggtcattgtg tcaattaagg taatgttagc
                                                                       480
 taatggatca aacacgatga gtttactaat aggagtatca gtcatttctg gctggatgca
                                                                       540
 atagctcata catgtaatcc cagtgctttg ggaggctgag cagagggatt gcttgacccc
                                                                       600
 660
                                                                       720
                                                                      721
<210> 100
<211> 645
<212> DNA
<213> Homo sapiens
<400> 100
cccccccc ccccaagac tgcaatgaca aatgctcaca caacaccgag gtcggggaga
cgcggagcag aactccagaa atgcctgccg tgtctgcgtt ctttagcctc gctgcgctgg
                                                                       60
ctgaagtggc agccatggaa aatgtgcaca gaggtcagag gtcaactccg ctcacccatg
                                                                      120
atggacagcc aaaagaaatg ccgcaggctc ctgtacttat ttcctgcgct gaccagtgaa
                                                                      180
gcgccctttc attgtaaaac attgtgcttt acctactacc ctagccttgt ctttaccgag
                                                                      240
ggatgctagt gagtccaagt ggtggaaaat atagactgca aacaagtgct tgttgcccca
                                                                      300
                                                                      360
cacggcccag attcacttga agcagaagtt agcatcctgg gccagtttgt tctctcagaa
cccagaatct ttgagggtaa ggttatctgt ctgatactga gcagaaacag aatgatcctg
                                                                      420
gagctttgct ttctattgaa ggcttttgac ggtaataggt ggtaacttgg taaaaggctg
                                                                      480
cctttactgt agctcaccca gcatctcttt taccaaccag agagtgtgaa actagtttca
                                                                     540
tatattacct agttattctt tcaaaacaaa acaaaaaaaa aaaaa
                                                                     600
                                                                     645
<210> 101
<211> 563
<212> DNA
```

<213> Homo sapiens

```
<400> 101
  ggcacgagat aagatcgcct taataccaga aatgattaga agtgctgatt tagattcaac
  aaataccata tgtccttatc attttttgta agaagaaatt ggttaagtcc taactttcaa
                                                                       60
  tgtgtaccca aatacttgta tttatgcttt tgataaaatg tatttcagc attaatacac
                                                                      120
  atccgattat gccttattta tatatgaaga ataaagttac catgttatac tgttatgtcc
                                                                     180
  taaaattcaa atcactattt gagaaaccct caaattggtg ctttcattat ataatgatac
                                                                     240
  atttagacaa aaccccaaac taagccattt gaaacaagat tetetecatt geagtttgta
                                                                     300
  gcaatgttat ttctgtgtat gtcatgagaa ggctaaatat cagtgttaat ttcttgtttg
                                                                     360
  aatccgtgaa atcatgcctg taaagcccaa acatttgtaa caaactccct aataaattta
                                                                     420
  480
  aaaaaaaaa aaaaaaaaa aaa
                                                                     540
                                                                     563
  <210> 102
  <211> 1324
  <212> DNA
  <213> Homo sapiens
 <400> 102
 gacagactgt tttttgcaag accacattat attactttat tattttctgc tttttcttt
 aacgacatta gtgtttttga tcactatatt ttaaaatgct ttttgtgagc cttttggtta
                                                                     60
 tgtggaatct gttccttagc tctgattttt tattcttatg gagcgtctta ggttactaca
                                                                    120
 tgaaggtaag actgccacag tcccccaggg aggcacactg tgttttactg attgatttga
                                                                    180
 agatgataga gagcctaggg ggatgagtct attggactca aaggttacat tttgtttttc
                                                                    240
 catttaattt aataatcaac aaaacgacaa agtcagttta atatctttct tctgctgagt
                                                                    300
 cttcaggatg ttagctagtc tttcaaaagc cattgctaca aaagtgcaaa tttctcattt
                                                                    360
 cctgtgggtc tctasaaact ctctcaatat ttaaagccaa acaaatccat cttttctgag
                                                                    420
 agacagaaac taaaaaattc agagttaatt cactattaaa aacagcaagg ccctgctatt
                                                                    480
 tcccaagaat aaagaaattt aaaattctca ttgtaagaag tatgaacttg aagctagaat
                                                                    540
 tggtttattt ctggcagcta cttacaatat taagaacttt actttttaaa tttgagacaa
                                                                    600
 tttcacagga aagcaagaaa ttagtctatt gtgaaatgtt tttacaacta acttggaata
                                                                    660
 tactgcaaat cactagtaag tagagacaca tttaagataa aatgattaat aaaacaattg
                                                                    720
 gtaattctga ataaggatct gaataaatcc agatcacaga ctgttccttt accaatatgt
                                                                    780
 aaaagaatgt gcaaaattmg taaaaatata cccaaaaatt taccagcaac agagaagcaa
                                                                    840
 agaatggagt tcaaccttac actataaaca tctaatagat atgtatgaaa atttaaaaac
                                                                    900
 tagaaaaggt tgggcatggt ggctcatgct tgtgatccca ggactttagg aggccaaggt
                                                                   960
 gggaggattg tttgagccca ggagttcaag accagcttga gcaatatagt gagaccctgt
                                                                  1020
 1080
 ggtgatgcac acctggagtc ctagctactc agaaggctga ggcaggacga tcacttgacc
                                                                  1140
 tcagaagtct gaggttacag tgagctatga tcataccagt gcactccagt ctgggtgaca
                                                                  1200
1260
                                                                  1320
                                                                  1324
<210> 103
<211> 1731
<212> DNA
<213> Homo sapiens
<400> 103
cccgggtcga cccacgcgtc cgtaaaattg aattttgcag actaaattat tttataaggc
tgttgctatt gaaagatcaa ttttgtcttt acctgcattt aaaatggaac agctcttagc
                                                                   60
agctgtggtt ttttttcca tattttttt aaatttgttg gctcttaaga tgaataaagt
                                                                   120
ttataggtgc atctgcctcc tcttctctaa gaatatgcat actaatgttt gtttctataa
                                                                  180
atcaaataca catgtgataa tatgcatgta aatacataac tatcctcatc atgtatggct
                                                                  240
ctcagttctt aattgatgat aacatgattg aattgccata tatctgtatt acttgtgtga
                                                                  300
atggttgtgt tgaacacgct aagaacaatt tgaattttat taagtacaaa aatccttaac
                                                                  360
                                                                  420
```

```
gtttgtatgg gaacattggc aagaaagaat agtgtgaaag ggaactgttt tagtttccta
                                                               480
tcagtaattg tacatgcagt taaatgttta aggtaaaatg attggtctct gtcacagcta
                                                               540
aaagatttca gtagccttca ttgagtttgg gtaaaataag ttgctgttct tttgtcttct
                                                               600
ttttaatata taaaagttat atttaaaaag tatataacat actatatatg ttacatacta
                                                               660
acatatatat acacaacaga aagtttattg gatttagtac tgatatttac tgtctatttt
                                                               720
780
agatatgtaa gtaaaggcaa gccctacaat tttaaaataa caaagcttat gtcttaagtt
                                                               840
gtattttttc aaaggttcat gtttttctga gtaaatgtgg tttattagca tgaaatatta
                                                               900
tgccttttac ttaaattatt ttatgtaaaa tagggcactg tttaattatg aaagggggaa
aatcattcca aataagagtt taattttat taattataaa aaactctgta ttagtttcct
                                                               960
agatgtgcta gaacaaatta ccacaaactg ggtggcttta aacaacagaa atttattctc
                                                              1020
                                                              1080
ttaacagttc cagagactaa atgtccagac tcacaatgtc ccagtgccat gcttcctcct
                                                              1140
taggccctag gaaagaatac ttcctagcct cttcctggct tttggtggtt gccagcaatc
                                                              1200
cetgetgtte ettageetat agtggettga etccaatete agttttgttg teaagtggte
                                                              1260
ttctaccctg tcttctatgt ttgtatccgt gtccaaactc tttttctagg gagaccagca
                                                              1320
ctggattaga gttcaccatg atccaatatg acctcatctt gactacatcc gcaaagaccc
                                                              1380
tgtctccaaa taaggtcaca tttacagggt accatgtgtt aggatttgac atatcttttg
                                                              1440
1500
gtgaagatta ctacctcttt tgatataact agtttctgag gtatttaaaa atttggtttt
                                                              1560
aaaaatatta agctttttgc tcatttgcat gtatactttt ctctcaacat tgttttggtt
                                                              1620
tatttaggtt atttgttaaa acttcagtaa atactaaagt tacttgtatt agaacataat
                                                              1680
1731
```

<210> 104 <211> 1466 <212> DNA

<213> Homo sapiens

<400> 104

ggcacgagct ctacctgaat gttcccctag agtttcatac acaatgtgtt ggaaacctaa 60 atgtatectt eteeteagtt ttgtatttea gtgtgtggea teateaacat ttgacecet 120 aggtagtgag agacettgga gtcaacetea atgteecate teetteeete teettateae 180 agggtgttgt tggttctcta tgtcccgggt ctcttaaaac cacctcttct cctccgcctc tacagacacc aacataaatc aagtttccat cttcgtttgc ctggacaagt ggcaaggcag 240 300 cactgaaagg atacteette etetagtett etetgeettt tgeetaetga geeeactett 360 ctgagctgct gataaaggaa tttacatacc acacatcctt tgatgggatt gccatgctac 420 aaagcagaac ctaaatccca tgcctggacg ttaggcagtc tacattctgg cttctgtgac 480 ttttggccta atttttgcat cagccccaaa tttctgttgt gccaccatcc cagtggattc 540 tagaatttag tottacacaa toattocata ttootttaat gagtoottta goatttgtto 600 attectttca tgtgeectat eccegtacet ggaattaett tteetetttt aettaeteaa 660 gtcctgcaaa agccagttcc attatgctgg tctcactgac ctctttctac atatttctgg 720 taagaatgaa ttactttctc ctgaaatacc tctgccatat tgtttaaaaa ttgccatatg 780 gtgctggaca tgagtatgtg ttcacatgtt tattatctac tctagtctca atttctaagg tettgaatat aggaaccaat ttatteatea eettatteea gacatgatgg aacteagett 840 tattgagaat caagtgatta tagtagatag tgaccatcct gagtatgttc atgtgttaca 900 960 taacaatgtt ttggtcaacc aaggactgca tataggaagg tgggctcata agattaatat ggagctgaaa aattcctaat gcttagccat atcgtagcca tgatattgta gcacaatgct 1020 1080 ttactcacge ggtgatgcta gtgtaaatgc tgccttacca gtcatataaa tgtatagcac aaggggccag gtggggtggc ttacacctgt aatctcagca ctttgggaag ctgaggggg 1140 aagattgctt gagcacagga atacaagtct agcctggtta atgtagggag ggcacgtttc 1200 tacaaaaact aaataaaatt agcctggcat ggtggcatgc acctgtagtc ccagctactc 1260 tggaggctga gacggaagga ttgtttgagt ccctggaggt tgagctgcag tgagccatga 1320 tcatgccact gcactccagt ctgggcgaca gagcaatccc ctttttcaaa aaaaaaaaa 1380 1440 aaaaaacaa aaaaaaaaaa aaaaaa

```
<210> 105
 <211> 1303
 <212> DNA
 <213> Homo sapiens
 <400> 105
 aggitaaatg cgtacttttc taacctttgt tattttgaaa gttattctga tattcctatc
                                                                          60
 cagttgtgcc tcatttacta gaaatttgct cacatggcca aatgatgtat ccacagaaca
                                                                         120
 atttgaaact agaccttttg gaagcgaact cctacaaact gtcatcaatg ttagcagaac
                                                                         180
 ttgagcaaag acctcaaccc agccatcctt gtagtaattc catcttcagg tggagggaaa
                                                                         240
 aggtaacatt taaggagact ggttgtaatt tcttgattgg gcctgctggg tggagtggct
                                                                         300
 taaagtagca tcagggcaaa aaaggtgtta ggaattctat gtgatattaa tattcatgca
                                                                         360
 gttagttaag aagataaatg ttttwatttt tcttttgagc acaataacaa gagctagaca
                                                                         420
 aaaccgaata cattctgtgt acaccaaact tctatgagaa gctaaaaaac acttttgatt
                                                                         480
 tettettet cateatacet gaattteate etttggatgt gettttacag taaaatttet
                                                                         540
 attaaattga aattttaata ttcgttcaga cctaaattat aagattttgt ggtatgtatt
                                                                         600
 agtctcatct gtttaagatg gtgcctaatg cagataatgc atcagtacag ctctgaaatg
                                                                         660
 cttgtagcta tttttattac tgatcagaag ggggaactgt aatcatcttg tgaagggaca
                                                                         720
 gttttctaag gctcaagagc tcgaaaacaa tctcaatcat ttacagggtt gtgatcattt
                                                                         780
cacttgcatt aagccaacta aagttgtatt tgtaaaagta atgctatgaa tattactatt
                                                                         840
 tgacctagac acataggtta gaattggaaa cacaggctat aaagtatagt aattgtgtaa
                                                                         900
 ttgtgaaaat attaaggctt caactcaaaa ctgaaacaca gtagggctta gaaatctttg
                                                                        960
aattatttat acccctcagt ttaaaaactt ccagtccagg cgcagtggct catgcctgta
                                                                        1020
atcccagaac tttgggaggc caaggcaggc ggatcacctg aggtcaggag ttcgagagca
                                                                        1080
gcctggctga cacggtgaaa ccccgtctct actaagaata caaaaattag ccaggcatgg
                                                                        1140
tggtgggcac ctgtaatccc agctacgggg gaggctgagg caggagaatc acttgaaccc
                                                                       1200
gggaggtgga ggttgtagtg ggccaagatc atgccactgc actccagcct gggtgaacag
                                                                       1260
ggcaagactc tgtctaaaaa aaaaaaaaaa aaaaactcgt agg
                                                                       1303
<210> 106
<211> 1516
<212> DNA
<213> Homo sapiens
<400> 106
ggcacgagag gaattgatgc tttaattttt ggatactttt tcagaatttt taatttacta
                                                                         60
tggtccggcc taagatcctc tgttgtatca ggttttgtgc acaaaagaaa agcacaaaag
                                                                        120
ttgaatgcac atggggcatg tgctttctgt gcaccaaata tctggatgag gttcttttt
                                                                        180
caggeetaca gteaaatetg tgteeagaat tttttgaett ttttgetttg tataateata
                                                                        240
gaattcattg ctgctgattt ctataatgat tcatgttgtc atgtgtctct taataactga
                                                                        300
gggctgtcag taacctgtga ttttgccttt tctatagtct tactcccatg aagaaccttg
                                                                        360
gttctgatgg agaaagtgaa aagctttatt tcttccccta gatatcttta tatttctatt
                                                                        420
atatttttta gttgtgtact gtgtactaga gattttttc agtttgttat gaacacaatt
                                                                        480
tggtaagccc taaattggtt ctgcctgtct ccaaacagaa acatctgtac aaatcttgtt
                                                                        540
ggtatagact actttctgga aaatggtcaa gataagttca tgttttcttg aaatttctaa
                                                                        600
gatagtatat ggtatcactt gtttaaagca aatcagactg agtttgacat ttaattcaat
                                                                        660
atttctggta ttcagtaacg ggtatatatg tttgttcttc cagtttgggt cagtttaaaa
                                                                        720
gatatgttgc aaagtataca tagaaaatgt gagcaatgcc tctctttgcc ttttgatcag
                                                                        780
aaacttcagc agagcggtaa ggattccaca tgatttaaac tgaaatgctt ttctttgttg
                                                                        840
ctgtaagaac ttaaaatgta aaataccttt ttcagtttaa gtcctgtaaa caacattgaa
                                                                        900
gcatggagat gaggcaagga atagtactca ctgaagttga aatgactgcc cacttcaaaa
                                                                        960
tcttcattgt gtttacacac cagtgtattt atacaaatca gaggcatttt gtagatgctt
                                                                       1020
tgctgacttg ttcagctctg taaaaacaca gaaatcagac ccattttgta aagcggaaaa
                                                                      1080
tcatgttaca tggaacatgt cctgtatata tcacatacat ggtaatggag tcttaatgat
                                                                      1140
aagtgcaaga taataattta atgatgggat tagtctgatc gcttaatatg cacaatcctg
                                                                      1200
gaagtgaatt acttgcatca gatatagtga tatttattat tetgtacaga gagaaaaata
                                                                      1260
```

```
catataaaac atatgcttac attacatgca cgcggatttc atgctccata atctttcta
                                                                       1320
 ttttttaatt tacctttctg taaatgatgt gcatggaata tgccttatag aaaaatgctg
                                                                       1380
 ttcataattt gactacgtgg aaaagtgcct atatggtggt aatgctagta aggcaaataa
                                                                       1440
 gacaaattat catgttggtt tactacatca ccagttaaca ttttatattg tgatgtttaa
                                                                       1500
 aaaaaaaaa aaaaaa
                                                                       1516
 <210> 107
 <211> 1689
 <212> DNA
 <213> Homo sapiens
 <400> 107
 actatagaag tcgcctgcag taccggctcc ggaattaagg gtcgacccac gcgtccgggc
                                                                        60
 taattgtttg gtcagaaatt cctaaggcca cagctttggg gggttcgtgt agatgtacat
                                                                       120
 ggtgggtggg ttataaatat tgggacttaa ggcagcttgt tctatgtatt tatctttgct
                                                                       180
 cttgggtgac ttagggaatg attttatttg atttaacctt ctttctgttt gccccgagaa
                                                                       240
 tactcgccag tggcgcttgc agttgtagca tttaccccaa gataactttg cctacgaaat
                                                                       300
 atttcgcttt tattatttyc acatcattct agtatatgga ctttggaaac aaaagacatt
                                                                       360
 gttctattta tagcattctt ttttttttt tagtagcggt atttccattt acaaaatata
                                                                       420
gtaactcttg attactgaaa atgtcaaatc ctagaaaacg tagcatgcct atacatgatg
                                                                       480
ttaacatcat tctcgaacag ttgttggccg aagattcatt tgatgaatcc aatttttttg
                                                                       540
aaatagacaa ttctgatgtt ctctttagaa ataactcagt ttttatcttt tttcacattg
                                                                       600
aaaatcagtt agatttgctt aagcctcaaa gagaatgttt atgtaaatta gcgctggcaa
ttttttttt tctaaacagg aaaagggtta aatgaaggtt gataaaatgg atgttcaatt
                                                                       660
                                                                       720
gtctttctga aagtgagtgg cttgaaggga tgaataaata ttttcttaat atattcaaaa
                                                                       780
aagtgcattg ctttctgtga tggaagttaa gacctaaatg tctggaagtt gtaaccctca
                                                                       840
acacagettt teetgatttg etgeaaagge acatagetga ttatagaagt gaagaeggea
                                                                       900
aggacgggga ctccaacaaa ggaaaccctg ttgcaggatt tgggaacttt catgcttcag
                                                                      960
atgaaattca ggcatgtgag catcactgca gaatgtggtg catcattgcc atcatgagta
                                                                     1020
atcacttgct gctcctactt ctgagaccaa gactcttttg tcatattctt tagcaatagg
                                                                     1080
acgggtaaag actggattta attgctgttc agagtataaa aactcaattg attccaacat
                                                                     1140
atctgaatgt gcagtaaagt cttaaaagtc aaccgttaat cattaagtct tttgcctcta
                                                                     1200
aagtettttg cetetgaaga agtttattae atgagttgat tttcatattt teattttggt
                                                                     1260
ggggttttcc tgttgttggg caaggtgggg tcacaggaca tgggactagt aagcatttta
                                                                     1320
ctgtttacta tatttgtctt tttataaaca gtatctccca aaatgtgatt agaaggctac
                                                                     1380
caageetgta tttggacatt taattgtgtg etttatataa tgtaaetaet aacagtattt
                                                                     1440
ggactgcctg ttcattcctg gagacaaaaa tgaaaatctg tcagttcaag ttcttgggta
                                                                     1500
acatcaagtc attagaattt atctaaagct tatcatgatt tgataagaca tccattgcat
                                                                     1560
gcagctgttt tagctcagtg caaaacactg aaattgtgat tcttagactg tttctgagac
                                                                     1620
1680
agggcggcc
                                                                     1689
<210> 108
<211> 1943
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (161)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (1926)
```

```
<223> n equals a,t,g, or c
  <220>
  <221> SITE
  <222> (1928)
  <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (1934)
 <223> n equals a,t,g, or c
 <400> 108
 ggcacgaggc ttggctaagg tccgcgggaa cccgtgagcc accgagagag cagagaactc
                                                                       60
 ggcgccgcca aacagcccag ctcgcgcttc aggtcccggc gccgtcgcgc actcctccga
                                                                      120
 tggccacaga tgtctttaat tccaaaaacc tggccgttca ngcacaaaag aagatcttgg
                                                                      180
 gtaaaatggt gtccaaatcc atcgccacca ccttaataga cgacacaagt agtgaggtgc
                                                                     240
 tggatgagct ctacagagtg accagggagt acacccaaaa caagaaggag gcagagaaga
                                                                     300
 tcatcaagaa cctcatcaag acagtcatca agctggccat tctttatagg aataatcagt
 ttaatcaaga tgagctagca ttgatggaga aatttaagaa gaaagttcat cagcttgcta
                                                                     360
                                                                     420
 tgaccgtggt cagtttccat caggtggatt atacctttga ccggaatgtg ttatccaggc
                                                                     480
 tgttaaatga atgcagagag atgctgcacc aaatcattca gcgccacctc actgccaagt
                                                                     540
 cacatggacg ggttaataat gtgtttgatc atttttcaga ttgtgaattt ttggctgcct
 tgtataatcc ttttgggaat tttaaacccc acttacaaaa actatgtgat ggtatcaaca
                                                                     600
 aaatgttgga tgaagagaac atatgagcac atgagttaag attgtgactg atcatgattt
                                                                     660
                                                                     720
 atttgaagat ggagcactgc tgatttatga aggaaaaaag aagaattttc taaagattac
                                                                     780
 acatatttca gaaagacttt acccaattca gttgtcagac ataatgattt atttgaaggc
                                                                     840
 ttgttttatt tgaagaaaag catattgcca aaaattctgg ttaaaagctt cctaacgggt
                                                                     900
 aacagaccat gggagagata tgtggttggg taatgcaaat gtagttatac aaagaaaaat
                                                                     960
 1020
 ggatatttct aacatgtaca aagctatgta ttttgattta ctttcatttc ttgctatgta
                                                                    1080
 tatgtacttt tcttaaaatg ccaagaactt tctcttgcta tcattgctcc ttttgaaaca
                                                                    1140
attcaatttt catgtctaca gctgactgtt ttgttaagat tgagtcatcg acattcagga
tttaagtctg aggtagtcaa ccctcaggaa aaaaaaaatg gcttatctga aatcagtact
                                                                    1200
                                                                    1260
gtggaaatga actatattag ctattatgaa taatgtccag tataagaata tgcttctgga
                                                                    1320
attgagttct ccttttaagt accaatgata cttaaatttc tcagaaatgt aatggtgtgt
                                                                    1380
cattgccttg aaatgcttgc ttagggcttc ttttatgtta tcttaaaaag tgctggtgaa
                                                                    1440
tittccattt tittacatcca tittcacatgt aagagacaaa aaagtctaga tiggtcttga
tattgagata ataaaaagta agtagcatta agaaaggtaa caatcttcat tctacagatg
                                                                    1500
                                                                    1560
aactcattga aacaatttag gggaatgagg ggcaaaaggg gagaaatact gctaaagaac
                                                                   1620
atgagcataa aaatgcgtgc gtttcagtgt ttaagaaggc ttgataaaga atgtcacttt
                                                                   1680
tttatttaac tgataagatt tttgttattt tttactttga taagtaaacc aaagaatatt
                                                                   1740
tgtatttcaa gcagtttgtg tggtgtttct atataatttt ctgtgtataa ataataaagt
aggcatttgt ttattttgta aaaaagaaat gaaaatctgc tggccagcta tgtcctctag
                                                                   1800
gaaatgacag acccaaccac cagcaataaa catttccatt gtcactgtaa aaaaaaaaa
                                                                   1860
                                                                   1920
aaaacncngg ggtncttttg ggg
                                                                   1943
<210> 109
<211> 1594
<212> DNA
<213> Homo sapiens
<400> 109
60
aatactttgc attaaaaatt tagatcttct tacatggaag aggtcaaatc cagttatagc
                                                                    120
aaaacacctt tactgcagag gccatataac caaaaagtcc aaaggcccag cccagtggac
```

catttacttc	agtgatgtto	agtacaaaat	: ttcactgcca	ttaaagactt	tggaaagtcc	240
ottttaagtt	gtaacaggat	: ttgactatta	gtgtggatt	cgataaccct	tctttagtta	300
acgcaacaa	tgctctttga	agctggaaat	atactggttt	cttgcaccct	tgtagttttc	360
tetgggettt	atgcaaaaga	tgtattttct	gaatgtctta	gtatgttgct	gtctttttac	420
craceragag	ftgccttcag	ı atgtgggtga	ggacttgttt	acaaaaagto	ctagaagacc	480
ttaagttaaa	attagetete	: caattttcaa	gtgttttctt	ttggcagaat	aagttttggg	540
tcctatgaga	ggtaaatagg	, ttggktgcct	ctcttgctat	agcccatcta	gagcagaaca	600
aaaactttgt	ttttgagggg	ı gatggagtta	ctttttacct	tgtcccctaa	ttgaatatat	660
ttaggacttt	tggttttaga	aatctcagag	ttctatagtt	ggaatagtgt	cacagagata	720
gtgttaggtt	tcttaggcaa	caaaattgga	gtgttaccta	ttgcccatct	gggcatggct	780
ttgatgagtt	ctatataaat	aatgagtgta	gcctaatttt	ctgtcatgtg	ctacctagca	840
tatacatttc	tgacagtcag	gtggattatc	ttgaaatttt	agacaaactt	tctgcctcct	900
tggaaagctc	tacatctcct	tgtgattgga	gtgtgggttt	caagattcca	gaargtgggt	960
gtmttcattt	tctattttca	atgcactcta	aagatgacct	gcttacaggt	tctctgaggc	1020
agacctcagt	tgctcttgtg	atatgtaact	ttgctttgat	aaggaataaa	caattacata	1080
tccagataat	gatacagaat	tgtcaaaatg	tttaatcatt	aagccactac	aaatagacat	1140
tttcgtggaa	taaactgatt	ttgaaatgtc	tttcaattta	tattgaaata	tctgaaggca	1200
cctctaaaat	ttgggtgatg	acacagaggt	atagattata	agatttaatt	atgaatgggt	1260
ggtatactgt	gaagactacg	gaagtgagca	gaaagatatg	tttggctttt	ttggttttta	1320
gttagagatt	ttaaaaaggt	ctgtgaaggt	caagttgatc	attggttttg	attgcatccc	1380
acaggtttct	ataaactggc	ttaaaaatgg	catactccat	tttctggtgt	attcattgta	1440
actttaggaa	gtatttgaaa	tggtcacatt	aaagtctagg	aatgtcaaat	tgtattttaa	1500
tgcgttagtt	ctttttcttt	ttctttttt	ttggagacag	cctgggcaac	aagagcaaaa	1560
ctctgtctca	aaaaaaaaa	aaaagggcgg	ccgc			1594
<210> 110						
<211> 1742						
<211> 1/42 <212> DNA						
<213> Homo	sapiens					
<400> 110						
ggcacgagct	cgtgccgctt	tgtagtctag	ggagtttaat	taaagtaagt	ппапасаваа	60
gtactctttt	gagagetgte	atttctctta	gtgtgacgct	attaataatg	tagtgtaatg	120
ctattttgga	agtttggttc	tttccttttc	ttttatcttc	ctctgactct	tttctctatt	180
ctaaatgaaa	ggggaataat	gcacttagag	gggggcactc	tcctaaattc	actototoat	240
gtacgacatt	atctccgact	tcggctctca	tgttttgaaa	aaatacctct	tcatcactct	300
atttttattt	ttcttcttct	tttattgtga	atctctttta	ccaaaaacat	ttatagggtt	360
cttcacaaag	atttttttt	tcaatcagga	tgaaaactag	atcatgatgt	Caccatttca	420
ctgtgagtgt	aacttccctt	tttgacagct	ccattagatc	taccagatta	taaatettea	480
tatttctgac	ttgccttgaa	atcagaaagt	gttttcatta	tactagtete	tataaacaac	540
aagcatgaag	gaaggcatgg	caggtatcat	agcccctttg	atgaacttac	Ctotttcaac	600
tcagtgccag	ggcagaacat	ttactgctaa	ccctgatggg	tcaactttga	ttgcaaarta	660
tgtgtggtac	attttgaatt	taaagaatgt	ttctgagatt	attctacgat	cacttotcat	720
ttttatgtgt	gcagtaatgt	gttgtgtata	acttggattt	caacaatatc	cattettea	780
aagttagaaa	atattctaag	aatactaatt	atcttgctca	aataatcatt	taagtacaac	840
tgtcacttga	ttatggtgaa	tatttttaag	taaaattata	tatttaaggt	atactacata	900
taattttatt	gtcatacaaa	aagcagatta	trgaacatgt	taatgtaaat	totactttta	960
attttttcca	gtactctaga	acatgtgtaa	ggttaaaaga	atttaaatta	cccacatttt	1020
tctttttaca	taataaataa	gaagaaatca	caaaggaagc	agatattata	ttatttttaa	1020
tatacacatg	aaattgtttg	actttatttt	gagacctcac	acaagtataa	acatoocao	1140
ggtgtgtatg	atcaaagtaa	gaaattaaag	agttaccogt	totttataaa	ccadaagtcc	1200
attgactttt	aataatocto	tctcaaatat	ttgatagtaa	attorogaaa	taatcaaacc	1260
tgagcctato	ggactgtact	ttgtagtact	atttaattta	ataactctaa	taatcootto	
agaatattag	gaaaaatagg	ccgggtgcag	tactcacccc	tataatoos	acactttcc	1320 1380
aggccgagga	gggcggatca	cctgaggtca	ggagttcaag	accatector	Ccaacateet	1440
gaaaacccat	ccctacaaaa	acacaataat	taggcaggca	tgatggtgag	tocctaraar	1500
			- 2222	2 22 2 2 3		

•	aaagaaaaag	attgcgccat	tacactccag aaagaatat	g cctgggcgad t aggaaaaat	c agagegaga a tettaatge	c ggaggttgca c tccctctcaa a aaatatatta a aaaaaaaaaa	1560 1620 1680 1740 1742
	<211> 1501 <212> DNA <213> Homo	sapiens					
	<400> 111						
	ggcacgagcc	tatttctgct	tactgtgtta	ccagagagco	: tgggggtctg	gatectatet	60
	tataaataa	gggtggattg	ccaaatgago	agttetette	cccagtccc	tttcctgtgc	120
	ctcttttaag	Coccatgett	attttcttat	gttattgaaa	tgagcactto	tgatttgggc	180
	ctactatcta	aagctatttg	agegreeate	cggtgcctgg	tgagggccct	gcatggctgg	240
	agaaagggtt	atatocaacc	ctatatetae	tastatas	ctatgtggct	taatttcaat	300
	tcactgcctg	Cttagaagta	aagttatgt	toccataag	gtttcaactt	tctgccagcg cacaattgag	360
	gtaattaacg	aaaattgtac	attggtggca	gcacctccta	taggatttgg	aatagtettt	420
	ctctagtaga	tcattggggg	ctcaccttga	tetectetet	tctatctacc	ctgcaccaaa	480
	ataccttgtc	ctgttttctg	gatatagttc	caataatttt	tttcctaaca	gcctttttgt	540 600
•	caccagttgg	tttgatatct	tacaacttgg	ccaaatgagg	gttccattaa	ctccatctto	660
	tctaatgcat	ggagaattca	aggattttt	ttttcctctt	ttcatagcac	cttccagttg	720
•	ccagttgtac	cctggccctt	ctttggaagt	cataatgatg	aatatccatt	aataagagat	780
	Lyatgetett	tcaactctca	tgtcatctat	accatctcag	tggagaggat	gactttggat	840
,	gaggiiggaa	tacaaaggaa	acatttggaa	gtccactgca	gtgtattata	tactatataa	900
•	aagtetgggg	gttaggaaat	acctggaggg	agaacttcct	aagaaatgat	ttttggttct	960
1	ttatttaaaa	aacagcacaa	taaaagtatc	ccatgagacc	attatgagca	ggacacgaca	1020
,	actoactass	ccctgggctg	tgactattta	cttctcggta	cagattactc	tggttaaatc	1080
,	attocatcto	acaacaaaat	catgeteaca	atctgaacct	gaaggctatt	actgaagaga	1140
į	ttcatttato	tttttaagtc	tattetetta	tccagagaaa	ggaccagaag	aaagtaaatt	1200
ć	acctgatgt	gatgggttcc	ttcagtcaac	aaaagattct	tttcccttaa	aaaataaaaa ttgtgtgcca	1260
ç	gatactottc	ttaatataaa	gatatggcac	tanaganaa	tgagcagtta	ttgtgtgcca ctttcgtcaa	1320
ç	cttacattc	tagtgaggaa	gataaccaaa	acaactcact	aatgtaccta	tcaaatgtca	1380
ē	ataaatgctg	tgaagaaaat	aaagtcagag	tattatatot	aaaaaaaaaa	ccaaatgtca	1440
ō	1	_	555	ou coucacy:	uuuuuaaaaa	aaaaaaaaa	1500 1501
							1501
< <	210> 112 211> 791 2212> DNA 2213> Homo	sapiens					
	400> 112						
9	gcacgaget	gcatttgatc	tcattctta	gtccaatgta	agtaagagta	aaacaatgac	60
a	icctaaggcc a	accaggctat	tctcattttt	ggaaaaatgc	tggattacat	taccagcata	120
·	.caaatgaga a	atatcaaggt	gtaatatctc	cctagaaatt	gtctcacctt	caatactatt	180
9	agetttcat	yacctgataa	ttttgttgtg	ggctctagcc	tcatgttata	ggaggtttac	240
<u>ح</u>	.aaactaaaa	tatatata	caccggatgt	gaatagcaca	ctccactacc	tacagcagta	300
t	taagaccat	regeolotaa . Ittattasss	acattgacaa	attgtccctg	gtagtgaaaa	tcacccctgg	360
t	gtatgttaa (roattaacat	taagagaat-	aactttcaca	tcaataaata	tgttaggctg	420
a	ttggggaat t	Lagtograca	ttatoctast	Lygagcaagc	actacatgaa	agcagtgacg	480
ŧ	catcctata d	agttt++c+	tagatttt	ayıladtata Cattagtata	gtgactgtaa acaggatgtt	tatctaaata	540
		, 5	guccecct	carragtata	acaggatgtt	grgtatgtta	600

```
cactgtatat actgttattt tgagagacaa ttttggggaat tttgccaagg tattttcaat
                                                                          660
 tataggtctt taatacattc taagcaagtg ggtctcaaaa atgggaattt tacaccccac
                                                                          720
 attettette ceateeggtg gaeatttgte aatgtgegea aatatttetg attaaaaaaa
                                                                          780
 aaaaaaaaa a
                                                                          791
 <210> 113
 <211> 1637
 <212> DNA
 <213> Homo sapiens
 <400> 113
 ggcacgagca ccactccctg ctcttctgca ccccaaatct tctttgttgg gaaaagaggt
                                                                          60
 aggagggagc tggctgggag gctcctagtc tgttgggaag cagtggatgg tggctcctct
                                                                         120
 ccatctcttc atccctttct cttggctagt gaggacaata gggcaattac tgagtcctgt
                                                                         180
 gggcaaggca ctgagtcatc ggtcgaatca gatgatgccc aggtcctggg gatgagtgag
                                                                         240
 tcactcttaa tgggcagctc ccaagatgaa tgttgagagc atcctgcctg gctttatgcc
                                                                         300
 tgcaagccct ccccgtaatc tccttccttc ttgcaggtgg gcaggaagaa gcagggtaga
                                                                         360
 aaagttagat teetaateta aeteetaeee eteaaeeeea agggaeettg ttggteaata
                                                                         420
 gcgaaggaac tggggaaggat gttcaaaggc tgaggcaggg cacagatgtc acatttcatc
                                                                         480
 tctgtggaag gtgggctgct caggccagat ggatgagctt gtttgtgtgt gaatgttcct
                                                                         540
 ctcaccttcc tgatggtgag gggggcgatg tccacttcca gatgctgcca agtagacttc
ctgttttctt cctcttgtcc ccccccgct tcctttttat atttacaaag ctctctggtt
                                                                         660
atgtacagca gggaaatggt gcctgagaga ctccttcaga tagcagttcc ttctagtttg
                                                                         720
agtcaggagg cactgcgtcc ccagagtccc tgcatcctca ttcatgaaat gctggcagtc
                                                                         780
aagggaacag ccctggctat ctcatgaggt tggccttagg atttaagtga gataatgtgt
                                                                         840
ttgacaatgg aatcccagca tgagcttggg tttcggcttc attaaaaaat tagaatttat
                                                                         900
tgtagaaaat ttagaaaata gacagaaaaa ataatcctag taccttctct tactatttga
                                                                         960
tgtatatccc atattttttt caaaaaaaag aaataatgat aataacatga tagtcatgta
                                                                       1020
tcaatgcatt ttctactttt gatggttaca ttattattat gtgagagaag gtcttatttg
                                                                       1080
tggagataac aactacaaaa agtatttggg ggggtgatgg agcatcaggt actcactcaa
                                                                       1140
atggttgaga gcaaaaagtt atttgtactg tactttttct taactttgtg aatattttga
                                                                       1200
aataaaagta cgtatgccat ttggagaaaa gaagatagca tagtggtggt tttttatgtc
                                                                       1260
tggaatatcc atgtctgtct attccagtgt ctggaatatc catgtctatc tatccactgg
                                                                       1320
aatatccagt gtctcagttg agggtactta aagggaaaaa cctcccacac ttgactttct
                                                                       1380
ttgaagagtt tacaaagatt tgtaatttca gcctgggcaa catggtgaga tcttgtctct
                                                                       1440
atatgaaata aaaaaattt aaaattagct ggatgtagtg atatgtgcct gtggtcctag
                                                                       1500
seettaggag getgaageea ggaggattge ttgageacag aagtteaagg etgeagtgag
                                                                       1560
ccatgaagtc tctcttgtat tccagcctgg gtgacagagc aagaccctga ctcaaaaaaa
                                                                       1620
aaaaaaaaa aaaaaaa
                                                                       1637
<210> 114
<211> 1588
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (778)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (1150)
<223> n equals a,t,g, or c
```

```
<400> 114
 gggaacgttt tcccagctga accacatgtg acgaaccaac ccatttatag tctaaaaatt
                                                                          60
 atgagaacaa gtctcttttt tttcttttt aaaaacatct tggtactttg tggtacattg
                                                                         120
 ctcatctcca gaagttccca ttcccagagt gccccgcgag gctgttggtg gccacataag
                                                                         180
 tgaccacagc aggccctgga atgcaagctc ttttccccgt ggctttggag cagaggggag
                                                                         240
 teagetgggt ggeettgtet eetgagggge attggeeagg gteacaeteg gttttetagg
                                                                         300
 gaccaggctg ttccatgggg tggagaggca gtaggccatc cctttctctt catctttat
                                                                         360
 ctagecette eccatacaaa caetttetea cagaaagaet tgtttgttgt eeeetgagea
                                                                         420
 aggccacage teteccacet atettetgtt caggttggca gatgggttca ggcaagggte
                                                                         480
 attctgagag gagacctcca cccaatgctc ccgtctgctg gcttggtcac cctgagctgc
                                                                         540
 tgcctgaggg gccaggaaag tggctggtgt ccccggcctg tgagagatgg ccagagcctc
                                                                         600
 agccagaccc accetgecag gagaaaaggg gagtggeegg agaagceace cettgagage
                                                                         660
 aggetggget egecettgtg eccaggaggg etgeacaggt geagttgeea ettteagace
                                                                         720
 acacacttca agctagagct tggcctgtgc ccctggtggt tgggggttgg aagarcanac
                                                                         780
 tgtgttgaca gggtctktaa ttcmcgattc caggtgcttc tgawttgttg gatcctgatg
                                                                         840
 aatcgcaatc aggactatgt ttggcttgag ctccagcctc atgaccacca accccatcga
                                                                         900
 atgactgaga gctgccaggc tcctgccacg ttggagctca saatcctccc gtggggacac
                                                                         960
 tgtgctgcag ccagcctcca gggagccgct tgttttatgg cctaaaaagt ctctttatgc
                                                                        1020
 tgagaaggtc acactggact ttgctcacac agagatttga cccaagaaaa ggaataaaga
                                                                        1080
 kgccttggat accctgtctt gcccctgttc ctgccccgc cgtaccctgc tggctcatgs
                                                                       1140
 cagaagamtn ggaacttgct gtctgtgggc atgtttgttg tcggctgamg gtagcaccca
                                                                       1200
 cagcactggc cgtgtgtgtg ccacagtcag gaacgargtc ctgccccca cccattaacc
                                                                       1260
 cattagettt gteettaete ettgaggeee tgettgaaaa gattaatggt getttgggar
                                                                       1320
 gctgaggcag gaggattgct tgaggccggg agctcgagac cagcctgggc gacatagcaa
                                                                       1380
 gaccetgtae etecaaaaaa taaaatataa acattagtea ggeatagagg cacacacaa
                                                                       1440
 cataggccta gctactcagc tgaggtagga ggattgcttg agcccaggag ttcaaggtta
                                                                       1500
 cagtgagcta tagtcatgcc atcatacact cagcctgggt gacagagtga gtccttgtct
                                                                       1560
 ctggaaaaaa aaaaaaaaa aactcgag
                                                                       1588
<210> 115
<211> 1926
<212> DNA
<213> Homo sapiens
<400> 115
taaccatgtt cttaacatct agatgcagaa atggatttga atgtgatctg cagtttctgt
                                                                         60
cgtagttatg aaatggcttt tgccaacatg ggttacccca aagcaaacat tgcatgctat
                                                                        120
ggaaatactt cttgtctctt tttctcccat ggtatctgta ttgcttcttt aataataaca
                                                                        180
tcatgtttta cagcctgcac tctgtgccca tgtttattca acccttttta ctttggtgac
                                                                        240
tgtttatcag atgtgttgcc ttgttcttcc tgccctccag agcccatgtt tttaattata
                                                                        300
actgaaatat gaaatgataa tatttgggct ttatttcttt tctttaaagg acagtactgc
                                                                        360
tttaaagaga cagtgttaag gatcttggaa gcacagccaa catgtgtgtg acatggaaga
                                                                        420
agccactaac caactcctag atgtgaacct acatgagaac cagaagtctg ttcaagtgac
                                                                        480
agaaagcgac ctcggaagtg aatctgagct tctagtcact attggagcca ctgtacctac
                                                                        540
tggctttgag caaacagctg cagatgaagt cagagagaaa cttgggtcat catgcaaaat
                                                                        600
cagcagagac cgtggcaaga tatattttgt catttcagtg gaaagtctgg cacaggtttg
                                                                       660
aatggagcaa tacttaaaat agttttctaa gttgatcatt ttatggttac ttttcatttt
                                                                       720
atagaccctt ctggaatcct ttctgatttt cattgctctg ccccaaatca ggtgatttta
                                                                       780
aagttactgc attttctatt gagtactgat ttgtaatttt gactgtagtt tcagtatccc
                                                                       840
ttaggaccaa aagtgtttca gatttttgga gggggttggg gggagttttg gaatatttgc
                                                                       900
attatacttg ccagttgagc atttctttt tttttctttt tctttgagac agagtcttgc
                                                                       960
totgtcatca ggctggagtg caatggcgcg atcttggctc actgcaacct ccgcctccca
                                                                      1020
ggttcaagca attctcctgc ctcagcctcc ccagtagctg ggactacagg cgcccgccac
                                                                      1080
cgcatctggc taatttttgt atatttagta gaaacggggt ttcaccatcc tggccaggct
                                                                      1140
ggtctcgaac tcctaacccc gtgatccacc cgcctcgacc tcccaaagtg ctgggattac
                                                                      1200
aggcctgagc cactgcgctc ggcctgccag ttgagcattt ctaatctgaa aatccgaaat
                                                                      1260
```

				64			
	gctgcactga	gcatttcctt	tcagcattg	t gttggggct	c aaaaagttt	agattttag	1320
	argragacta	ctcaacctgt	agtaggatt	g ctacatttt	t agaggtgate	tagtatttct	1320
	cyayyattga	attcaccaga	aagaatact	g ttcaacttaa	gaaattetet	aagtatotos	1440
	gractiatit	acttcagcat	atagcagat	g tttaacctt	. ggtgatgaaa	Catagaaga	1500
	attiteettt	taatttgcat	: caaaaattc	t tgctcagaad	i taattaggad	tcactcaaga	1560
	caaaaagtga	aggtcagaaa	actgcaatc	t cactatcata	a aagctgatat	atctcattac	1620
	Cacataagca	gtgagagggc	: aaggattgt:	t gtctatttt	ttttccacca	atatatocca	
	cyclettagt	gtctggcata	tagtaggta	ccagaaaata	i totataaaa	gaattggtaa	1680
	gcaaatgttt	tccatccaat	. attttagcca	a ataccctcac	r cagetttgto	aagatagga	1740
	ctattattat	cctcattaat	cattaggcti	t aggacacata	aataattcc	ccagggccac	1800
	tcagctagta	atcacagaac	tggageteaa	a atcccctoca	. 2222222222	aaaaaaaaa	1860
	aaaaaa					aaaaaaaaa	1920
							1926
	<210> 116						
	<211> 1063						
	<212> DNA						
	<213> Homo	sapiens					
		•					
	<400> 116						
	ccacgcgtcc	gaggagaaca	agtggactco	ggtagcttct	250005		
	tgtggctgtg	gctgtgttag	gagggttctt	atatgctgta	acyagtacca	gaagactagg	60
	tcctctcaac	acagtggaac	gttacaatco	tcaggaaaac	ggrggererg	acgggacatc	120
	tatggggacc	Cggaggaaac	acctargeto	tgcagtatat	agauggcaca	ctatagcccc	180
	aggaggtaga	gatgacacta	cagagetg	cagtgctgag	caggacatga	tctatgctgt	240
	ccagtggtct	Ccagtggtgg	ccatgacatg	acgccgtagt	agatacaacc	ccagaaccaa	300
	caatggacag	Ctcatoocao	taggaggttt	tgatggcaca	ggagttggcc	tggcagtggt	360
	agtttttgat	CCtgatgcca	atacatogag	gttatatggc	acatacttga	agaccataga	420
	agggggtggc	gtaggagtta	ttaaaatgac	gualatgge	gggatgaatt	accgtcggct	480
	gagaagacag	tettetatatat	attectetet	acattgtgaa	tcccatattt	ggtgaacaca	540
	tacagettga	gaaaacatta	caacaaattt	attctgggga tattatttgc	gctttgacct	tggagctttg	600
	atacaatcca	atgaaagtac	ttcacctace	actactige	cggtgcctca	acaaatggaa	660
	aagaatattt a	atttttaatt	ttaatttato	agatgcacaa	taattttcaa	ctctgtgcag	720
	atcetteete	Cacaaaaa	agaaaagaag	atggttttt	gttgttttcg	ttttgaactt	780
	atcetteete d	atteatttae	ayaaaayaay	aaaaaattcc	aagcagcaaa	acttactttg	840
	tttgtaaggt a	attattteta	gilligaaaat	actatttaat	aagggcagaa	gggctatata	900
•	tgatttggct a	accacticcia	gacactccat	ccacatgatt	ccactaacaa	ggattaccag	960
	gaataaaggt a	atcttanana	aatgtattag	ctacccatta	ttctcgcact	aaccaccaga	1020
	agacttgaaa a	acccidadaa	aaaaaaacaa	aaaaaaaaa	aaa		1063
	<210> 117						
	<211> 1615						
	<212> DNA						
	<213> Homo s						
	12137 HOMO S	abrens					
	<400> 117						
	ggcacgagct c	grgccgctt	aagtttacag	gttcagatag	cttttctcac	accataggac	60
	tegretatea t	ttttgtgta	gtttttcttt	tttaatatgg	cttotcttat .	Cagatttest	120
	gctatiggtt c	cctccctta	ttccacctgg	cccttctttt	tctttatctt -	ttt=tt++	180
	cccigictaa c	ttttattcc	attttctcca	ctttcttctt	tctgtgagcc :	ataccetaes	240
	adayaacccc a	grgggccag	agttgagatg	caaattotta	dactactota .	~~~~	300
	cccaciccat a	ttggcaaag .	ccagaaatcc	tgactgtttt	acttoctott .	at anna t	360
	cccaccitat t	.cccaggga	atatcttctg	tctactttaa .	atatgattcc :	2722777	420
	ccacciccay c	adattactc	tgccttccct	gtacactttc .	aaatttoota /	TOOCOL OLL	480
	catataaagt g	gaaggtete a	atctctaaat	ttctagtaga ;	atccaactaa :	333030355	540
	cccgagetga g	accettete	tgagcaaagg	aactcaccca (gtcactcttt /	inaantttaa	600
	agtcgtgctc t	ttgtacgta	tcatatatac	tatgaacttg	ttttctcctc a	ittgaaagat	660
				-	-	-3946	550

```
aagatgtcag ctttgcatgt ttcctttatt ccagtggaga tccttcaggg tttggtgagt
ggaaatctgg gaggcacact tgggccgact gtcagcagcc ccattgagca agatgtggtc
                                                                    720
agtcccgttt ccctgccccg gagagcaaag acctttggag gatttgacag ccgcttcagc
                                                                    780
aaggtggtga ctattctggt aactatggtt acaataatga caaccaggaa ttttatcagg
                                                                    840
atacttatgg gcaacagtgg aagtagacaa gtaagggctt gaaaatgata ctggcaagat
                                                                    900
acgattggct ctagatctac attcttcaaa aaaaaaaatt ggcttaactg tttcatcttt
                                                                    960
aagtacattt tgctgccatt tgtattgggc tgaagaaatc actattgtgt atatactcaa
                                                                   1020
gtctttttat ttttcctctt ttcataaatg ctcttggaca ttattgggct tgcagagttc
                                                                   1080
ccttattctg gggattacaa tgcttttatc gtttcaggct tcattttagc ttcaaaacaa
                                                                   1140
gctgggcaca ctgttaaatc atgattttgc agaacctttg gttttggaca gtttcatttt
                                                                   1200
tttggatttg ggatagatta cataggagta tggagtatgc tgtaaataaa aatacaagct
                                                                   1260
agtgctttgt cttagtagtt ttaagaaatt aaagcaaaca aatttaagtt ttcttgtatt
                                                                   1320
gaaaataacc tatgattgta tgttttgcat tcctagaagt aggttaactg tgtttttaaa
                                                                  1380
ttgttataac ttcacacctt tttgaaatct gccctacaaa atttgtttgg cttaaacgtc
aaaagccgtg acaatttgtt ctttgatgtg attgtatttc caatttcttg ttcatgttaa
                                                                  1500
1560
                                                                  1615
<210> 118
```

```
<211> 1221
  <212> DNA
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (697)
  <223> n equals a,t,g, or c
  <220>
  <221> SITE
  <222> (700)
 <223> n equals a,t,g, or c
  <220>
 <221> SITE
 <222> (701)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (712)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (720)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (722)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (742)
<223> n equals a,t,g, or c
```

<400> 118

66

PCT/US98/27059

```
cactagtgga tccaaagaat tcggcacgag gagagacttg catagatcag ggagtatgtg
                                                                         60
 aaaataaatg tcagttgcca gagaaagaat agatcaaaca gtttatttga atttctgatg
                                                                        120
 agtttggtga ggaagtgtat agcacttaac atttggaagg cagacaaaag gttttgttgt
                                                                       180
 tggtgttatg ttccttttga attttagata cataatgcga ttttttttct ggccaatgct
                                                                       240
 ccaggcaaaa ttgatgtctt tccactttct aaaacccatc atatttatga actctctgat
                                                                       300
 actetgtetg aaacagtegt geteetgtga ggttgaaata teteteetge etetateaca
                                                                       360
 gcagacgcac agaactgatc tgggattttc tcactcagga tcccaaaatg agccctttct
                                                                       420
 caatcttgac aaacgtgcag cagaagccca ttgtgcagtt atggttctgt gcctgctggg
                                                                       480
 cagggattta aaggccagga gaagcaggga aggccctgct ctctgctcca gccaggtggt
                                                                       540
 aatatgcatt ctcaaactag ctaggaaaag gttctagatt cctttgaatc tattgctgaa
                                                                       600
 tcccactgat tagcttttcc cactgacaga cattcaaatc tttgtttttg gagcttcctc
                                                                       660
 tgcagacttg gtgtaaattt caaaaaaaga aaacaangcn ntgaagctta anacaggcan
                                                                       720
 anacagttgg cttcctacct angcatgctt caaactcact atatgacttg gtaaattctg
                                                                       780
 ttactttaat gcatgcttgt tttcacatgt gtaaaatgag agagtatcag actagatcat
                                                                       840
 900
 cttttataaa agttaagtgg ccgggagctg tggcccatgc ctgtaatccc agcactttag
                                                                       960
 gaggccgaag cgggtggatc acctgaggtc gggagttcaa gaccagcctg accaacatgg
                                                                      1020
 agaaaccctg tctttactaa aaatacaaaa aattaggcag gcatggcggt gcatgcctgt
                                                                      1080
 aatcccagct actcgggagg ctgaggtagg agaatcgctt gaacctggga ggcagaggtt
                                                                      1140
 gcggtgagcc gagatcatgt ccattgcact ccagcctggg caacaagaac aaaaatccgt
                                                                      1200
 ctcaaaaaaa aaaaaaaa a
                                                                      1221
 <210> 119
 <211> 1149
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (1120)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (1140)
<223> n equals a,t,g, or c
<400> 119
gggtttctgg ggattggatt caaagagcag aagtatgatg ccaggggctg gtaaggactc
                                                                       60
agccatatag agatttcagc tgcattataa tgtatatttg agaaattgag ttcttattat
                                                                      120
cagaaaattg acctatgtaa tgaaatacta gaagaaaact ctaaattaga atggctttgt
                                                                      180
tatgaatttt taatgataag tactaacact taaaagggaa aaaatttttc aaagaaaatg
                                                                      240
cctaaaaatg tgttgtatct gagatcatca tatatgtagt attacagtgc aaacactatt
                                                                      300
aatgttaatg aggtaggtgg atttttttaa tgaaaaaact tgaaatatta tcaggttgtc
                                                                      360
cccatttatg gaatttaagc ttgtcagaaa gatccagata gctatattaa tattttatct
                                                                      420
gtatttggtt gcggttgctt ttaaaaaataa gttttcttat aagtcatttc aattttttgg
                                                                      480
tttagagtcc atatttcaaa ataaaaagtt aaaaaaagag taccttatgt aatttagcaa
                                                                      540
ggtattccat aaactcaggg aggaaaaaaa aaaaactaag atgagaggct agttataatg
                                                                      600
atctttattt atatattgca ggaaatgatt tcctctctca caacttagca taatttactg
                                                                      660
ctaatatttt tagccatggg ttgaaaaaaa ttaartggtt ttgtaagtgc taatcctttg
                                                                      720
ttactcattt aaactggtaa aatgtagtcc ccgctccctg aggaggacct gtccaaactc
                                                                      780
ttcaaaccac cacageegee tgccaggatg gactegetge teattgcagg ecagataaac
                                                                      840
acttactgcc agaacatcaa ggagttcact gcccaaaact taggcaagct cttcatggcc
                                                                     900
caggetette aagaatacaa caactaagaa aaggaagttt eeagaaaaga agttaacatg
                                                                      960
```

```
aactcttgaa gtcacaccag ggcaactctt ggaagaaata tatttgcata ttgaaaagca
  cagaggattt ctttagtgtc attgccgatt ttggctataa cagtgtcttt ctagccataa
                                                                       1020
  taaaataaaa caaaatettg aaaaaaaaaa aaaaaaaaan gggsggccgc tetaaggggn
                                                                       1080
                                                                       1140
  tccaagctt
                                                                       1149
  <210> 120
  <211> 1515
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (69)
 <223> n equals a,t,g, or c
 <400> 120
 aattcggcac gagggaaatt caagcacttt tcctaaaaga agggggaatg gatgctgaaa
 caacacgint cccacaaagg gagcagacac tgggcttgtg aagctgcccc ataccttccc
                                                                        60
 cacagaactg gggtccggcc tccctgacat gcagatttcc acccagaaga cagagaagga
                                                                       120
 gccagtggtc atggaatggg ctggggtcaa agactgggtg cctgggagct gaggcagcca
                                                                       180
 cegtttcage ctggccagee ctctggacee cgaggttgga ccctactgtg acacacetae
                                                                       240
 catgoggaca ctcttcaacc toototggct tgccctggcc tgcagccctg ttcacactac
                                                                       300
 cctgtcaaag tcagatgcca aaaaagccgc ctcaaagacg ctgctggaga agagtcagtt
                                                                       360
 ttcagataag ccggtgcaag accggggttt ggtggtgacg gacctcaaag ctgagagtgt
                                                                       420
ggttcttgag catcgcagct actgctcggc aaaggcccgg gacagacact ttgctgggga
                                                                       480
tgtactgggc tatgtcactc catggaacag ccatggctac gatgtcacca aggtctttgg
                                                                       540
gagcaagttc acacagatct cacccgtctg gctgcagctg aagagacgtg gccgtgagat
                                                                       600
gtttgaggtc acgggcctcc acgacgtgga ccaagggtgg atgcgagctg tcaggaagca
                                                                       660
tgccaagggc ctgcacatag tgcctcggct cctgtttgag gactggactt acgatgattt
                                                                       720
ccggaacgtc ttagacagtg aggatgagat agaggagctg agcaagaccg tggtccaggt
                                                                       780
ggcaaagaac cagcatttcg atggcttcgt ggtggaggtc tggaaccagc tgctaagcca
                                                                       840
gaagcgcgtg accgaccage tgggcatgtt cacgcacaag gagtttgagc agctggcccc
                                                                      900
cgtgctggat ggtttcagcc tcatgaccta cgactactct acagcgcatc agcctggccc
                                                                      960
                                                                     1020
taatgcaccc ctgtcctggg ttcgagcctg cgtccaggtc ctggacccga agtccaagtg
gcgaagcaaa atcctcctgg ggctcaactt ctatggtatg gactacgcga cctccaagga
                                                                     1080
tgcccgtgag cctgttgtcg gggccaggta catccagaca ctgaaggacc acaggccccg
                                                                     1140
gatggtgtgg gacagccagg yctcagagca cttcttcgag tacaagaaga gccgcagtgg
                                                                     1200
gaggcacgtc gtcttctacc caaccctgaa gtccctgcag gtgcggctgg agctggcccg
                                                                     1260
ggagctgggc gttggggtct ctatctggga gctgggccag ggcctggact acttctacga
                                                                     1320
cctgctctag gtgggcattg cggcctccgc ggtggacgtg ttctttcta agccatggag
                                                                     1380
1440
                                                                     1500
aaaaaaaaa aaaaa
                                                                     1515
<210> 121
<211> 1025
<212> DNA
<213> Homo sapiens
<400> 121
ggagaattgt tactggtgaa ttggttttca ggttttgagc atacatatac aatgtgtttc
aaatgctgct tgtaaaatta aaccatcatc tagaatagag ttaatttatt ataatcaagc
                                                                       60
tacaaatagg ttttcttaaa ccagagatgc actgcccttg tctaaagttc ttattgcact
                                                                      120
ggtttatatg tgtatgtgtg ttttattgtg tgttttttta atttgtaagt attctaagag
                                                                      180
tttcctaata ctaaggitaa aattttcatg ttgacctgag ccttttgcaa atttgctttg
                                                                      240
gctctattga tttgtccatt atgtgttagg caaatataac ttaagtggag ggggaagttt
                                                                      300
                                                                      360
```

```
atgaatataa tatagetetg tgttttaaae etcagaaaca gatttgagtg tttcagtatt
                                                                  420
atagaaacag tgatgactat tcatgctctg ctagtctatg cctgcaactc caaatgtttg
                                                                  480
tggttcagta tttcccacct acatttctgt ttggtgacat tgctcatttt aacaaatatg
                                                                  540
accgagtcta gttttccttt aaaaggatag tttatgagta atctttaaaa ccatttccat
                                                                  600
accatctgta tataaccatt tcggtagaga acacactaca ctgaaccctg ctttagagct
                                                                  660
gtgtgttgag ctaaaaatat aatttttaa aaattgacta gcaaaatcta tggccacact
                                                                  720
gagaageett tgaaaatgge aaataetttt cateaceaat tgeecaatte atetttette
                                                                 780
tgcttcctca gccttgtagc aaaggctaca cagcagccca cagtccacag tctttttggg
                                                                 840
aaaattggcc tgccaccttc tttaagctca gtttattttt gacttacttt ctttgctgta
                                                                 900
gttatgaacc ttggggcatt aaaatcccat ggcaaggagc ataagagatg ttctcgtagc
                                                                 960
1020
tcgag
                                                                1025
```

<210> 122 <211> 2207 <212> DNA

<213> Homo sapiens

<400> 122

ggcacgagca cgaatcagct gcaggtctct gttttgaaaa agcagagata cagaggcaga 60 ggaaaagggt ggactcctat gtgacctgtt cttagagcaa gacaatcacc atctgaattc 120 cagaagccct gttcatggtt ggggatattt tctcgactgc atggaatcag aaagaagcaa aaggatggga aatgcctgca ttcccctgaa aagaattgct tatttcctat gtctcttatc 180 240 tgcgcttttg ctgactgagg ggaagaaacc agcgaaccaa aatgccctgc cgtgtgtact 300 tgtaccaaag ataatgcttt atgtgagaat gccagatcca ttccacgcac cgttcctcct 360 gatgttatct cattatcctt tgtgagatct ggttttactg aaatctcaga agggagtttt 420 ttattcacgc catcgctgca gctcttgtta ttcacatcga actcctttga tgtgatcagt 480 gatgatgctt ttattggtct tccacatcta gagtatttat tcatagaaaa caacaacatc 540 aagtcaattt caagacatac tttccgggga ctaaagtcat taattcactt gagccttgca 600 aacaacaatc tccagacact cccaaaagat attttcaaag gcctggattc tttaacaaat 660 gtggacctga ggggtaattc atttaattgt gactgtaaac tgaaatggct agtggaatgg 720 cttggccaca ccaatgcaac tgttgaagac atctactgcg aaggcccccc agaatacaag 780 aagcgcaaaa tcaatagtct ctcctcgaag gatttcgatt gcatcattac agaatttgca 840 aagtotcaag acctgootta toaatcattg tocatagaca otttttotta tttgaatgat 900 gagtatgtag tcatcgctca gccttttact ggaaaatgca ttttccttga atgggaccat 960 gtggaaaaga ccttccggaa ttatgacaac attacaggca catccactgt agtatgcaag 1020 cctatagtca ttgaaactca gctctatgtt attgtggccc agctgtttgg tggctctcac atctataagc gagacagttt tgcaaataaa ttcataaaaa tccaggatat tgaaattctc 1080 aaaatccgaa aacccaatga cattgaaaca ttcaagattg aaaacaactg gtactttgtt 1140 gttgctgaca gttcaaaagc tggttttact accatttaca aatggaacgg aaacggattc 1200 tactcccatc aatccttaca cgcgtggtac agggacactg atgtggaata tctagaaata 1260 1320 gtcagaacac ctcagacact cagaacgcct catttaattc tgtctagtag ttcccaacgt 1380 cctgtaattt atcagtggaa caaagcaaca caattattca ctaaccaaac tgacattcct aacatggagg atgtgtacgc agtgaagcac ttctcagtga aaggggacgt gtacatttgc 1440 1500 ttgacaagat tcattggtga ttccaaagtc atgaaatggg gaggctcctc gttccaggat 1560 attcagagga tgccatcgcg aggatccatg gtgttccagc ctcttcaaat aaataattac 1620 caatatgcaa ttcttggaag tgattactcc tttactcaag tgtataactg ggatgcagag 1680 aaagccaaat ttgtgaaatt tcaggaatta aatgttcagg caccaagatc attcacacat 1740 gtgtccatta ataagcgtaa ttttcttttt gcttccagtt ttaagggaaa tacacagatt 1800 tacaaacatg tcatagttga cttaagcgca tgagacacca aattctgtgg ctgccatcag 1860 aaattttcta cagtacatga cccggatgaa ctcaatgcat gatgactctt cttatcacac 1920 ttgcaaatga atgcctttca aacattgaga ctgctagaac caagcactac cagtatctcc 1980 atccttaact gtccagtcca gtgatgtggg aagttacctt ttataagaca aaatttaatt 2040 gtgtaactgt tctttgcagt gaagatgtgt aaataagcgt ttaatggtat ctgttactcc 2100 aaaaagaaat attaatatgt acttttccat ttatttattc atgtgtacag aaacaactgc 2160 caaataaaat gtttacattt tctttcataa aaaaaaaaa aaaaaaa 2207

```
<210> 123
  <211> 1770
  <212> DNA
  <213> Homo sapiens
  <400> 123
  gctgagtgtg agctgagcct gccccaccac caagatgatc ctgagcttgc tgttcagcct
  tgggggcccc ctgggctggg ggctgctggg ggcatgggcc caggcttcca gtactagcct
                                                                            60
  ctctgatctg cagageteca ggacacetgg ggtctggaag geagaggetg aggacaceag
                                                                           120
  caaggacccc gttggacgta actggtgccc ctacccaatg tccaagctgg tcaccttact
                                                                           180
  agetetttge aaaacagaga aatteeteat ceactegeag cageegtgte egeaggaget
                                                                           240
  ccagactgcc agaaagtcaa agtcatgtac cgcatggccc acaagccagt gtaccaggtc
                                                                           300
  aagcagaagg tgctgacctc tttggcctgg aggtgctgcc ctggctacac gggccccaac
                                                                           360
  tgcgagcacc acgattccat ggcaatccct gagcctgcag atcctggtga cagccaccag
                                                                          420
  gaacctcagg atggaccagt cagcttcaaa cctggccacc ttgctgcagt gatcaatgag
                                                                          480
  gttgaggtgc aacaggaaca gcaggaacat ctgctgggag atctccagaa tgatgtgcac
                                                                          540
  cgggtggcag acagcctgcc aggcctgtgg aaagccctgc ctggtaacct cacagctgca
                                                                          600
  gtgatggaag caaatcaaac agggcacgaa gttccctgat agatccttgg agcaggtgct
                                                                          660
  gctaccccac gtggacacct tcctacaagt gcatttcagc cccatctgga ggagctttaa
                                                                          720
  ccaaagcctg cacagcctta cccaggccat aagaaacctg tctcttgacg tggaggccaa
                                                                          780
  ccgccaggcc atctccagag tccaggacag tgccgtggcc agggctgact tccaggagct
                                                                          840
  tggtgccaaa tttgaggcca aggtccagga gaacactcag agagtgggtc agctgcgaca
                                                                          900
 ggacgtggag gaacgcctgc acgcccagca ctttaccctg caccgctcga tctcagagct
                                                                          960
 ccaagccgat gtggacacca aattgaagag gctgcacaag gctcaggagg ccccagggac
                                                                         1020 -
 caatggcagt ctggtgttgg caacgcctgg ggctggggca aggcctgagc cggacagcct
                                                                        1080
 gcaggccagg ctgggccagc tgcagaggaa cctctcagag ctgcacatga ccacggcccg
                                                                        1140
 cagggaggag gagttgcagt acaccctgga ggacatgagg gccaccctga cccggcacgt
                                                                        1200
 ggatgagatc aaggaactgt actccgaatc ggacgagact ttcgatcaga ttagcaaggt
                                                                        1260
 ggagcggcag gtggaggagc tgcaggtgaa ccacacggcg ctccgtgagc tgcgcgtgat
                                                                        1320
 cctgatggag aagtctctga tcatggagga gaacaaggag gaggtggagc ggcagctcct
                                                                        1380
 ggageteaae eteaegetge ageaeetgea gggtggeeat geegaeetea teaagtaegt
                                                                        1440
 gaaggactgc aattgccaga agctctattt agacctggac gtcatccggg agggccagag
                                                                        1500
 ggacgccacg cgtgccctgg aggagaccca ggtgagcctg gacgagcggc ggcagctgga
                                                                        1560
 cggctcctcc ctgcaggccc tgcagaacgc cgtggacgcc gtgtcgctgg ccgtggacgc
                                                                        1620
 gcacaaagcg gagggcgagc gggcgcgggc ggccacgtcg cggctccgga gccaagtgca
                                                                        1680
 ggcgctggat gacgaggtgg gcgcgctgaa
                                                                        1740
                                                                        1770
<210> 124
<211> 1034
<212> DNA
<213> Homo sapiens
<400> 124
ggcacgagga aagtacgagt cggctcagcc tggagggacc caaccagagc ctggcctggg
agccaggatg gccatccaca aagccttggt gatgtgcctg ggactgcctc tcttcctgtt
                                                                         60
cccaggggcc tgggcccagg gccatgtccc acccggctgc agccaaggcc tcaacccct
                                                                        120
gtactacaac ctgtgtgacc gctctggggc gtggggcatc gtcctggagg ccgtggctgg
                                                                        180
ggcgggcatt gtcaccacgt ttgtgctcac catcatcctg gtggccagcc tcccctttgt
                                                                        240
gcaggacacc aagaaacgga gcctgctggg gacccagcta agaggccggt gtcaccatac
                                                                        300
agegggtaca atgggcaget getgaceagt gtgtaceage ceaetgagat ggeeetgatg
                                                                        360
cacaaagttc cgtccgaagg agcttacgac atcatcctcc cacgggccac cgccaacagc
                                                                        420
caggrgargg gcagrgccaa crcgacccrg cgggcrgaag acargracrc ggcccagagc
                                                                        480
caccaggegg ccacacegee gaaagaegge aagaaetete aggtetttag aaaeeeetae
                                                                        540
gtgtgggact gagtcagcgg tggcgaggag aggcggtcgg atttggggag ggccctgagg
                                                                        600
                                                                        660
```

acctggcccc	gggcaaggga	ctctccaggc	tectectece	cctagaaa	ccagcaacat	
gtgccccaga	tgtggaaggg	CCECCEE	******	ccrygcagge	ccagcaacat	720
CCCCacccac	tecterate		raccagtatt	tgggtgggtg	ccagcaacat tcatgggtgt	780
		LLYLYVAULU	uaddaaccaa	000000000		
	5	ugccadalau	LOTTCTCGGG	ataataa.		840
atgtttctct	ggagattcct tgaggaacaa	gcaacctcaa	Cacacataca	aragragety	ggcagcgcct	900
tgctcctcta	tgaggaagaa	grate	gagacttccc	aggcgctcag	gcctggatct	960
aaaaaaaaa	3-33-4444	gggrgcctaa	taaatacatt	tctgctttat	taaaaaaaa	1020
uuuuuaaaaa	aaaa					
						1034

<210> 125

<211> 353

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (353)

<223> Xaa equals stop translation

<400> 125

Met Leu Cys Arg Leu Cys Trp Leu Val Ser Tyr Ser Leu Ala Val Leu 1 5 10 15

Leu Leu Gly Cys Leu Leu Phe Leu Arg Lys Ala Ala Lys Pro Ala Glu 20 25 30

Thr Pro Arg Pro Thr Ser Leu Ser Gly Ala Pro Pro Thr Pro Arg His 35 40 45

Ser Arg Cys Pro Pro Asn His Thr Val Ser Ser Ala Ser Leu Ser Leu 50 55 60

Pro Ser Arg His Arg Leu Phe Leu Thr Tyr Arg His Cys Arg Asn Phe 65 70 75 80

Ser Ile Leu Leu Glu Pro Ser Gly Cys Ser Lys Asp Thr Phe Leu Leu 85 90 95

Leu Ala Ile Lys Ser Gln Pro Gly His Val Glu Arg Arg Ala Ala Ile 100 105 110

Arg Ser Thr Trp Gly Arg Trp Gly Asp Gly Leu Gly Pro Ala Leu Lys
115 120 125

Leu Val Phe Leu Leu Gly Val Ala Gly Ser Ala Pro Pro Ala Gln Leu 130 135 140

Thr Glu Asp Phe Phe Asn Leu Thr Leu Lys Glu Leu His Leu Gln Arg 165 170 170

Asp Asp Val Phe Val His Val Pro Asn Val Leu Glu Phe Leu Asp Gly

195

205

Trp Asp Pro Ala Gln Asp Leu Leu Val Gly Asp Val Ile Arg Gln Ala

200

Leu Pro Asn Arg Asn Thr Lys Val Lys Tyr Phe Ile Pro Pro Ser Met 230

Tyr Arg Ala Thr His Tyr Pro Pro Tyr Ala Gly Gly Gly Tyr Val 250

Met Ser Arg Ala Thr Val Arg Arg Leu Gln Ala Ile Met Glu Asp Ala 260 265

Glu Leu Phe Pro Ile Asp Asp Val Phe Val Gly Met Cys Leu Arg Arg

Leu Gly Leu Ser Pro Met His His Ala Gly Phe Lys Thr Phe Gly Ile 295

Arg Arg Pro Leu Asp Pro Leu Asp Pro Cys Leu Tyr Arg Gly Leu Leu

Leu Val His Arg Leu Ser Pro Leu Glu Met Trp Thr Met Trp Ala Leu 330

Val Thr Asp Glu Gly Leu Lys Cys Ala Ala Gly Pro Ile Pro Gln Arg

Xaa

<210> 126

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (108)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (156)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (158)

<223> Xaa equals stop translation

<400> 126

Met Ser Trp Val Gly Leu Gly Arg Arg Gly His Leu Leu Leu Ile

Asn Pro Arg Ala Leu Ala Gly Ile Arg Leu Pro Ser Pro Thr Gly Ala 20

Pro Ala Pro Gly Pro Cys Pro Pro Leu Cys Thr Pro His Cys Ser Arg

Glu His Pro Ala Gly Gly Thr Gly His Pro Ala Gly Val Trp Trp Arg 50 55

Arg Gly Cys Tyr Gly Gly Ser Cys Pro Met Gly Pro Val Arg Gly Ile

Leu Gly Gly Leu Pro Cys Arg Glu Glu Ala Leu Arg Arg His His Ser

Lys Pro Cys Trp Arg Pro Gly Gly Gln Ala Arg Xaa Leu Gly Ser Trp 100

Pro Leu Thr Ala Gly Arg Glu Pro Pro Arg Thr Ala Ser Thr Ala Pro

His Thr Ser Glu Pro Thr Ser Ser Phe Pro Arg Phe Pro Arg Ser Gln 130 135 140

Ala Trp Glu Asp Leu Pro Asp Ala Ala His His Xaa Ser Xaa 150

<210> 127

<211> 554

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (39)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (199)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (201)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (202)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (228)

<223> Xaa equals any of the naturally occurring L-amino acids

```
<220>
 <221> SITE
  <222> (420)
 <223> Xaa equals any of the naturally occurring L-amino acids
  <220>
  <221> SITE
 <222> (434)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (440)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (452)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (554)
 <223> Xaa equals stop translation
 <400> 127
 Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu
                                      10
 Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
              20
                                  25
Phe Gln Ala Phe Met Lys Xaa Gly Lys Leu Phe Cys Pro Gln Asp Lys
Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
                                      90
Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
            100
                                 105
Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
                            120
Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
    130
                        135
Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val
```

SUBSTITUTE SHEET (RULE 26)

155

															10
									74						
Cys	Ser	Ala	Phe	165	Pro	Phe	Val	Arg	Asp 170	Gly	/ Arc	, Leu	Gly	Cys 175	Thr
Arg	Glu	Asn	180	Pro	Val	Leu	Gly	Pro 185	Asp	Gly	Lys	Thr	His 190		' Asn
Lys	Cys	Ala 195	Met	Суз	: Ala	Xaa	Leu 200		Xaa	Lys	Glu	Ala 205		Asn	Ala
Lys	Arg 210	Glu	Gly	Glu	Thr	Arg 215	Ile	Arg	Arg	Asn	Ala 220		Lys	Asp	Phe
Cys 225	Lys	Glu	Xaa	Glu	Lys 230	Gln	Val	Arg	Asn	Gly 235	Arg	Leu	Phe	Cys	Thr 240
Arg	Glu	Ser	Asp	Pro 245	Val	Arg	Gly	Pro	Asp 250	Gly	Arg	Met	His	Gly 255	Asn
Lys	Cys	Ala	Leu 260	Cys	Ala	Glu	Ile	Phe 265	Lys	Gln	Arg	Phe	Ser 270	Glu	Glu
Asn	Ser	Lys 275	Thr	Asp	Gln	Asn	Leu 280	Gly	Lys	Ala	Glu	Glu 285	Lys	Thr	Lys
Val	Lys 290	Arg	Glu	Ile	Val	Lys 295	Leu	Cys	Ser	Gln	Tyr 300	Gln	Asn	Gln	Ala
Lys 305	Asn	Gly	Ile	Leu	Phe 310	Cys	Thr	Arg	Glu	Asn 315	Asp	Pro	Ile	Arg	Gly 320
Pro	Asp	Gly	Lys	Met 325	His	Gly	Asn	Leu	Cys 330	Ser	Met	Cys	Gln	Ala 335	Tyr
Phe	Gln	Ala	Glu 340	Asn	Glu	Glu	Lys	Lys 345	Lys	Ala	Glu	Ala	Arg 350	Ala	Arg
Asn	Lys	Arg 355	Glu	Ser	Gly	Lys	Ala 360	Thr	Ser	Tyr	Ala	Glu 365	Leu	Cys	Ser
Glu	Туг 370	Arg	Lys	Leu	Val	Arg 375	Asn	Gly	Lys		Ala 380	Cys	Thr .	Arg	Glu
Asn 385	Asn	Pro	Ile	Gln	Gly 390	Pro	Asp	Gly	Lys	Val 395	His	Gly	Asn '		Cys 400

SUBSTITUTE SHEET (RULE 26)

Ser Met Cys Glu Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys

Lys Glu Gly Xaa Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser

Phe Xaa Glu Leu Cys Ser Glu Xaa Arg Lys Ser Arg Lys Asn Gly Arg

Leu Phe Cys Xaa Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys

455

425

415

430

460

405

435

75

Met His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Glu 465 470 475 480

Glu Arg Ala Arg Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys 485 490 495

Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg 500 505 510

Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys 515 520 525

Cys Ala Met Cys Ala Ser Val Phe Lys Leu Glu Lys Lys Lys Lys Lys 530 540

Lys Lys Lys Lys Gly Arg Pro Leu Xaa 545 550

<210> 128

<211> 308

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (308)

<223> Xaa equals stop translation

<400> 128

Met Asn Thr Val Leu Leu Ser Leu Leu Phe Ser Leu Pro Arg Ile Val

1 5 10 15

Tyr Ala Met Ala Ala Asp Gly Leu Phe Phe Gln Val Phe Ala His Val

His Pro Arg Thr Gln Val Pro Val Ala Gly Thr Leu Ala Phe Gly Leu
35 40 45

Leu Thr Ala Phe Leu Ala Leu Leu Leu Asp Leu Glu Ser Leu Val Gln 50 55 60

Phe Leu Ser Leu Gly Thr Leu Leu Ala Tyr Thr Phe Val Ala Thr Ser
65 70 75

Ile Ile Val Leu Arg Phe Gln Lys Ser Ser Pro Pro Ser Ser Pro Gly
85 90 95

Pro Ala Ser Pro Gly Pro Leu Thr Lys Gln Gln Ser Ser Phe Ser Asp 100 105 110

His Leu Gln Leu Val Gly Thr Val His Ala Ser Val Pro Glu Pro Gly

Glu Leu Lys Pro Ala Leu Arg Pro Tyr Leu Gly Phe Leu Asp Gly Tyr 130 135 140

76

Ser Pro Gly Ala Val Val Thr Trp Ala Leu Gly Val Met Leu Ala Ser 145 150 155 160

Ala Ile Thr Ile Gly Cys Val Leu Val Phe Gly Asn Ser Thr Leu His 165 170 175

Leu Pro His Trp Gly Tyr Ile Leu Leu Leu Leu Leu Thr Ser Val Met 180 185 190

Phe Leu Ser Leu Leu Val Leu Gly Ala His Gln Gln Gln Tyr Arg

Glu Asp Leu Phe Gln Ile Pro Met Val Pro Leu Ile Pro Ala Leu Ser 210 215 220

Ile Val Leu Asn Ile Cys Leu Met Leu Lys Leu Ser Tyr Leu Thr Trp 225 235 235

Val Arg Phe Ser Ile Trp Leu Leu Met Gly Leu Ala Val Tyr Phe Gly 245 250 255

Tyr Gly Ile Arg His Ser Lys Glu Asn Gln Arg Glu Leu Pro Gly Leu 260 265 270

Asn Ser Thr His Tyr Val Val Phe Pro Arg Gly Ser Leu Glu Glu Thr 275 280 285

Val Gln Ala Met Gln Pro Pro Ser Gln Ala Pro Ala Gln Asp Pro Gly
290 295 300

His Met Glu Xaa 305

<210> 129

<211> 167

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (167)

<223> Xaa equals stop translation

<400> 129

Met Ala Ala Ala Val Leu Ala Met Thr Leu Ala Pro Thr Val Ser Gly

1 5 10 15

Thr Thr Ser Lys Cys Ser Ser Arg Arg Trp Cys Pro Val Pro Ala Ser 20 25 30

Ser Ser Cys Val Ser His Leu Leu Gly Ser Gly Cys Ala Pro Cys Ala 35 40 45

Pro Trp Thr Ala His Pro Arg Gln Pro Ser Gln Cys Trp Ser Ala Arg 50 55 60

77

Ala Pro Arg Arg Leu Gly Ser Arg Pro Arg Arg Tyr Leu Leu Thr Gly 65 70 75 80

Gln Ala Asn Gly Ser Leu Ala Met Trp Asp Leu Thr Thr Ala Met Asp 85 90 95

Gly Leu Gly Gln Ala Pro Ala Gly Gly Leu Thr Glu Gln Glu Leu Met 100 105 110

Glu Gln Leu Glu His Cys Glu Leu Ala Pro Pro Ala Pro Phe Ser Ser 115 120 125

Leu Met Gly Leu Ser Pro Gln Pro Leu Thr Pro His Leu Pro His Gln 130 135 140

Pro Lys Pro Pro Ala Gly Xaa 165

<210> 130

<211> 306

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (306)

<223> Xaa equals stop translation

<400> 130

Met Ala Ala Gly Leu Ala Arg Leu Leu Leu Leu Gly Leu Ser Ala 1 5 10 15

Gly Gly Pro Ala Pro Ala Gly Ala Ala Lys Met Lys Val Val Glu Glu 20 25 30

Pro Asn Ala Phe Gly Val Asn Asn Pro Phe Leu Pro Gln Ala Ser Arg
35 40 45

Leu Gln Ala Lys Arg Asp Pro Ser Pro Val Ser Gly Pro Val His Leu 50 55 60

Phe Arg Leu Ser Gly Lys Cys Phe Ser Leu Val Glu Ser Thr Tyr Lys
65 70 75 80

Tyr Glu Phe Cys Pro Phe His Asn Val Thr Gln His Glu Gln Thr Phe 85 90 95

Arg Trp Asn Ala Tyr Ser Gly Ile Leu Gly Ile Trp His Glu Trp Glu 100 105 110

Ile Ala Asn Asn Thr Phe Thr Gly Met Trp Met Arg Asp Gly Asp Ala 115 120 125

78

Cys Arg Ser Arg Ser Arg Gln Ser Lys Val Glu Leu Ala Cys Gly Lys
130 135 140

Ser Asn Arg Leu Ala His Val Ser Glu Pro Ser Thr Cys Val Tyr Ala 145 150 155 160

Leu Thr Phe Glu Thr Pro Leu Val Cys His Pro His Ala Leu Leu Val 165 170 175

Tyr Pro Thr Leu Pro Glu Ala Leu Gln Arg Gln Trp Asp Gln Val Glu 180 185 190

Gln Asp Leu Ala Asp Glu Leu Ile Thr Pro Gln Gly His Glu Lys Leu 195 200 205

Leu Arg Thr Leu Phe Glu Asp Ala Gly Tyr Leu Lys Thr Pro Glu Glu 210 215 220

Asn Glu Pro Thr Gln Leu Glu Gly Gly Pro Asp Ser Leu Gly Phe Glu 225 235 240

Thr Leu Glu Asn Cys Arg Lys Ala His Lys Glu Leu Ser Lys Glu Ile 245 250 255

Lys Arg Leu Lys Gly Leu Leu Thr Gln His Gly Ile Pro Tyr Thr Arg 260 265 270

Pro Thr Glu Thr Ser Asn Leu Glu His Leu Gly His Glu Thr Pro Arg 275 280 285

Ala Lys Ser Pro Glu Gln Leu Arg Gly Asp Pro Gly Leu Arg Gly Ser 290 295 300

Leu Xaa 305

<210> 131

<211> 220

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (56)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (58)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (204)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (209)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (220)

<223> Xaa equals stop translation

<400> 131

Met Pro Cys Leu Glu Ala Val Ala Leu Ile Leu Leu Ile Leu Leu Val 1 5 10 15

Pro Asp Pro Pro Arg Gly Ala Ala Glu Thr Gln Gly Glu Gly Ala Val
20 25 30

Gly Gly Phe Arg Ser Ser Trp Cys Glu Asp Val Arg Tyr Leu Gly Lys
35 40 45

Asn Trp Ser Phe Val Trp Ser Xaa Leu Xaa Val Thr Ala Met Ala Phe 50 55 60

Val Thr Gly Ala Leu Gly Phe Trp Ala Pro Lys Phe Leu Leu Glu Ala 65 70 75 80

Arg Val Val His Gly Leu Gln Pro Pro Cys Phe Gln Glu Pro Cys Ser 85 90 95

Asn Pro Asp Ser Leu Ile Phe Gly Ala Leu Thr Ile Met Thr Gly Val

Ile Gly Val Ile Leu Gly Ala Glu Ala Ala Arg Arg Tyr Lys Lys Val

Ile Pro Gly Ala Glu Pro Leu Ile Cys Ala Ser Ser Leu Leu Ala Thr

Ala Pro Cys Leu Tyr Leu Ala Leu Val Leu Ala Pro Thr Thr Leu Leu 145 150 155 160

Ala Ser Tyr Val Phe Leu Gly Leu Gly Glu Leu Leu Ser Cys Asn 165 170 175

Trp Ala Val Val Ala Asp Ile Leu Leu Ser Val Val Val Pro Arg Cys
180 185 190

Arg Gly Thr Ala Glu Ala Leu Gln Ile Thr Val Xaa His Ile Leu Gly 195 200 205

<210> 132

<211> 99

<212> PRT

<213> Homo sapiens <220>

<221> SITE

<222> (99)

<223> Xaa equals stop translation

<400> 132

Met Met Asn Gln His Leu Leu Glu Ser Phe Gly Ser Pro Ser Ser Leu

Phe Ile Val Phe Ile Leu Leu Ile Trp Met Leu Gln Arg Cys Lys Asp

Phe Phe Leu Cys Cys Tyr Arg Val Val Leu Thr Pro Ser Phe Trp Gln 40

Lys His Gln His Pro Asp Pro Lys Ile Lys His His Leu Lys Leu Tyr

Ser Leu Lys Tyr Ser Ser Ser Gly Gln Asn Asn Phe Arg Lys Asp Lys

His Trp Leu Ser Gly His Thr Glu Glu Ala Asn Leu Ile Lys Glu Glu 90

Trp Lys Xaa

<210> 133

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (61)

<223> Xaa equals stop translation

Met Thr Ser Ser Leu Phe Ile Phe Leu Phe Leu Trp Phe Cys Pro Pro

Pro Arg Ile Ser Phe Val Leu Cys Trp Pro Gln Pro His Ser Gln Val

His Ile Gln His Glu Lys Ala Asp His Leu Phe Gln Ser Leu Lys Gln

Lys Ala Pro Gly Leu Leu Gln Trp Ala Arg Ile Val Xaa 55

<210> 134

<211> 248

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (14)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (141)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (248)

<223> Xaa equals stop translation

<400> 134

Met Ala Val Pro Ala Leu Thr Pro Ala Ala Val Arg Ala Xaa Gly Leu 1 5 10 15

Leu Gly Val Ser Trp Thr Trp Ala Leu Phe Thr Pro Leu Val Ala Leu 20 25 30

Gly Arg Glu Gly Ser Gln Asp Ser Ala Thr Thr Pro Ser Arg Pro 35 40 45

Pro Gly Arg Pro Arg Ile Val Asp Ile Ala Thr Ile Val His Cys Tyr 50 55 60

Ala Glu Glu Arg Gln Ser Ala Glu Asp Tyr Glu Lys Glu Glu Ser His
65 70 75 80

Arg Gln Arg Arg Leu Lys Glu Arg Glu Arg Ile Gly Glu Leu Gly Ala 85 90 95

Pro Glu Val Trp Gly Pro Ser Pro Lys Phe Pro Gln Leu Asp Ser Asp 100 105 110

Glu His Thr Pro Val Glu Asp Glu Glu Glu Val Thr His Gln Lys Ser 115 120 125

Ser Ser Ser Asp Ser Asn Ser Glu Glu His Arg Lys Xaa Lys Thr Ser 130 135 140

Arg Ser Arg Asn Lys Lys Lys Arg Lys Asn Lys Ser Ser Lys Arg Lys 145 150 155 160

His Arg Lys Tyr Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp Thr Asn 165 170

Ser Asp Ser Asp Asp Asp Lys Lys Arg Val Lys Ala Lys Lys Lys Lys Lys 180 185 185

Lys Lys Lys Lys His Lys Thr Lys Lys Lys Lys Asn Lys Lys Thr Lys 195 200 205

82

Lys Glu Ser Ser Asp Ser Ser Cys Lys Asp Ser Glu Glu Asp Leu Ser 210 215 220

Glu Ala Thr Trp Asp Gly Ala Ala Lys Cys Gly Arg Tyr Tyr Gly Phe 225 230 235 240

Asn Arg Ala Arg Ser Thr Tyr Xaa 245

<210> 135

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (41)

<223> Xaa equals stop translation

<400> 135

Met Val Cys Phe Tyr Ala Leu Leu Cys Phe Leu Ser Ser Val Glu
1 5 10 15

Ile Gly Pro Leu Ser Trp Leu Leu Cys Leu Ser His Ile Lys Cys His 20 25 30

Phe Thr Ala Leu Pro Phe Glu Ala Xaa 35 40

<210> 136

<211> 75

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (75)

<223> Xaa equals stop translation

<400> 136

Met Leu His Leu Phe Cys Ser Gln Pro Leu Gly Leu Leu Phe Leu Leu 1 5 10 15

Ile Phe Leu Gly Leu Asp Ser Leu Pro Arg Cys Leu Thr Ala Thr Arg 20 25 30

Leu Gln Ser Pro Ile Ile Ile Phe Ser Thr Leu Ser Cys Ile Cys Ser 35 40 45

Thr Ser Trp Leu Glu Leu Cys Ser Val Tyr Phe Leu Thr Leu Asn Tyr 50 55 60

Leu His Val Val Pro Pro Cys Phe Leu Ile Xaa 65 70 75

```
<210> 137
 <211> 75
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (75)
 <223> Xaa equals stop translation
 <400> 137
 Met Gly Val Leu Thr Arg Glu Leu Phe Gly Val Val Gly Met Leu Tyr
 Ile Leu Ile Val Gly Met Val Thr Trp Leu Asp Ala Phe Val Lys Thr
                                   25
 His Leu Met Val Met Gln Asn Glu Tyr Ile Leu Phe Tyr Val Asn Tyr
 Thr Ser Lys Leu Asn Phe Phe Lys Lys Phe Leu Leu Lys Ser Lys Asp
 Ile Cys Gly Ala Ser Cys Lys Phe Tyr Cys Xaa
                      70
<210> 138
 <211> 58
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (58)
<223> Xaa equals stop translation
Met Lys Val Leu Leu Ser Leu Ser Leu Val Gly Leu Phe Ile Gly Phe
                                      10
Ser Asp Ala Val Leu Asn Glu Thr Cys Arg Phe Trp Ile Asn Thr Ser
                                 25
Ser Lys Gly Asn Leu Gln Ile Leu Lys Asn Gln Ile Gln Ile Ile Asp
Arg Leu Arg Lys Met Pro Ala Ser Ala Xaa
    50 ...
                         55
<210> 139
<211> 173
<212> PRT
<213> Homo sapiens
```

```
WO 99/31117
                                      84
 <220>
 <221> SITE
 <222> (76)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (124)
<223> Xaa equals any of the naturally occurring L-amino acids
Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe Leu
Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu Glu Glu
                                  25
Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala Val Pro Cys
                             40
Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys Lys Glu Leu Gln
Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly Xaa Ser Ser Pro Ala
Gln Pro Pro Asp Pro Pro Arg Met Gly Glu Val Arg Ile Ala Ala Glu
                 85
Glu Gly Arg Ala Val Val His Trp Cys Ala Pro Phe Ser Pro Val Leu
His Tyr Trp Leu Leu Trp Asp Gly Ser Glu Xaa Arg Arg Arg Gly
       115
                            120
```

Pro Pro Leu Asn Ala Thr Val Arg Arg Ala Glu Leu Lys Gly Leu Lys

Pro Gly Gly Ile Tyr Val Val Cys Val Val Ala Ala Asn Glu Ala Gly 145 155

Ala Ser Arg Val Pro Gln Ala Gly Gly Glu Gly Leu Glu 165

<210> 140 <211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (46)

<223> Xaa equals stop translation

Met Thr Ile His Ala Leu Leu Val Tyr Ala Cys Asn Ser Lys Cys Leu

10

15

5

Trp Phe Ser Ile Ser His Leu His Phe Cys Leu Val Thr Leu Leu Ile

Leu Thr Asn Met Thr Glu Ser Ser Phe Ser Leu Lys Gly Xaa 35 40 45

<210> 141

<211> 58

1

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (58)

<223> Xaa equals stop translation

<400> 141

Met Val Tyr Arg Ala Phe Leu Ile Ile Leu Arg Phe Ile Leu Ile 1 5 10 15

Phe Leu Phe Lys Leu Asn Tyr Ser Lys Leu Cys Pro Glu Ile Pro Phe 20 25 30

Gly Leu Lys Phe Phe Ser Phe Val Cys Ile Lys Val Gln Ile Lys Lys
35 40 45

Thr Ser Arg Lys Arg Arg Pro Tyr Leu Xaa 50 55

<210> 142

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (67)

<223> Xaa equals stop translation

<400> 142

Met Phe Val Glu Arg Trp Leu Pro Cys Phe Leu Val Val Ala Val Val 1 5 10 15

Val Trp Val Phe Ala Cys Gly Pro Val Glu Asp Lys Glu Asp Ser Phe 20 25 30

Gly Trp Ser Ser Tyr Phe Leu Ala Ser Gly Leu Pro Pro Leu Leu Phe

Glu Ala Ser Gln Thr Arg Thr Val Arg Ala Gly Arg Leu Gly Val Phe
50 55 60

Val Cys Xaa

```
65
```

```
<210> 143
 <211> 53
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (53)
 <223> Xaa equals stop translation
 <400> 143
 Met Ile Phe Lys Leu Leu Ile Phe Arg Ile Phe Phe His Glu Leu Ala
                                      10
 Leu Ala Leu Cys Ile Ser Asn Leu Val Ser Leu Pro Trp Leu Ser Tyr
             20
 Phe Trp Cys Pro Glu Met Gln Asn Leu Phe Leu Leu Asp Thr His Ile
                              40
 Trp Val Leu Met Xaa
     50
<210> 144
<211> 66
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (66)
<223> Xaa equals stop translation
<400> 144
Met Val Leu Ser Val Ala Leu Leu His Ala Leu Ser His Leu Met Pro
                 5
                      . 10
Cys Lys Thr Cys Leu Ala Ser Thr Ser Pro Ser Ala Met Ile Val Ser
                                 25
Phe Leu Arg Pro Pro Gln Pro Ala Met Trp Asn Cys Glu Ser Ile Lys
Pro Phe Leu Phe Ile His Tyr Pro Val Ser Gly Ser Ile Phe Ile Ala
                        55
Val Xaa
65
```

<210> 145 <211> 57 <212> PRT

```
<213> Homo sapiens
  <220>
  <221> SITE
  <222> (57)
  <223> Xaa equals stop translation
  <400> 145
 Met Val Ala Ile Leu Leu Arg Glu Leu Pro Leu Ala Phe Leu Leu Val
 Gly Ser Ser Gly Asp Lys Phe Cys Phe Thr Ser Ser Glu Asn Val Leu
               20
                                   25
 Leu Ser Phe Ser Phe Leu Lys Asp Ile Phe Ala Gly Tyr Lys Asn Ser
 Gly Leu Met Val Leu Phe Ile Val Xaa
      50
 <210> 146
 <211> 67
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (67)
 <223> Xaa equals stop translation
 <400> 146
Met Ser Asn Phe Ile Ser Ile Thr Cys Leu Val Phe Thr Ile Leu Gly
                   5
His Leu Val Ser Leu Gln Val Ala His Ser Ser Val Phe Glu Phe Lys
                                  25
Thr Leu Tyr Val Leu Lys Thr Asn Arg Tyr Ser Gln Ser Leu Phe Arg
                              40
His Phe Cys His Leu Ser Phe Ile Arg Thr Arg Lys Ile Phe Leu Lys
                         55
                                              60
Asn Asn Xaa
 65
<210> 147
<211> 49
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (49)
<223> Xaa equals stop translation
```

40 45

Xaa

```
<210> 148
<211> 89
<212> PRT
<213> Homo sapiens
<220>
```

<221> SITE <222> (89)

<223> Xaa equals stop translation

Ile Lys Tyr Thr Cys Phe His Leu Val Phe Gly Gln Ile Pro Val Thr 20 25 30

Val His Val Asn Ile Trp Gln His Lys Asn Val Thr Phe Phe Ile Leu 35 40 45

His Cys Gly Ile Pro Ala Leu Thr Arg Asp Ser Ala Ala Leu Thr Tyr 50 55 60

Ser Asn Asp Gly Thr Val Ile Glu Thr Leu Leu Phe Leu Ile Leu Tyr
65 70 75

Leu Asp Leu Asn Ile Ile Cys Cys Xaa 85

<210> 149 <211> 77 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (77)

<223> Xaa equals stop translation

<400> 149
Met Thr Leu Tyr Ser Lys Leu Leu Trp Leu Phe Lys Gly Glu Leu Leu

5 10

Phe Pro Leu Val Leu Ala Tyr Val Leu Leu Leu Tyr Ile Val Thr Lys

Phe Asn Tyr Leu Ile Leu Lys Leu Phe Pro Asn Lys Ile Gln Ile Lys 35 40 45

Arg Gly Ser Ile Ala Ser Asn Arg Ser Leu Glu Ser Ser Ala Ser Leu 50 55 60

Pro Ala Arg Lys Glu Glu Lys Leu Leu Lys Lys Phe Xaa 65 70 75

<210> 150 -

<211> 42

1

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals stop translation

<400> 150

Met Asn Leu Ser Phe Leu Ser Phe Phe Leu Phe Phe Tyr Leu Leu Trp

1 10 15

Ser His Ser Ile Val Glu Lys Ile Lys Xaa 35 40

<210> 151

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (46)

<223> Xaa equals stop translation

<400> 151

Met Asn Ala Leu Pro Asn Leu Ala Trp Leu Pro Phe Val Pro Ala Leu

1 5 10 15

Ala Ala Ala Ser Pro Ala Gly Leu Ala Ala Pro Glu Ser Arg Asp Val 20 25 30

Pro Phe Pro Val Ser Pro Ala Thr Gln Leu Asn Ile Gly Xaa 35 40

```
90
  <210> 152
  <211> 42
  <212> PRT
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (42)
  <223> Xaa equals stop translation
  <400> 152
 Met Leu His Leu Cys Leu Gly Leu His Leu Val Pro Pro Gly Leu
 Leu Ser Val Asn Ser Leu Gln Ser Thr Gln Cys Ser Leu Phe Ser Ala
              20
                                   25
 Ala Lys Phe Phe Ser Ile Val Gln Val Xaa
 <210> 153
 <211> 44
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (44)
 <223> Xaa equals stop translation
 <400> 153
Met Pro Tyr Met Phe Arg Pro Ala Phe Leu Asn Cys Gly Thr Phe Ala
Ile Phe Gly Gln Leu Asn Ser Val Val Gly Ala Val Leu Cys Ile Ala
              20
                                  25
Gly Cys Leu Ala Ala Ser Leu Ala Ser Thr Tyr Xaa
         35
<210> 154
<211> 123
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (123)
<223> Xaa equals stop translation
<400> 154
Met Pro Pro Leu Ala Pro Gln Leu Cys Arg Ala Val Phe Leu Val Pro
                                     10
```

SUBSTITUTE SHEET (RULE 26)

Ile Leu Leu Leu Gln Val Lys Pro Leu Asn Gly Ser Pro Gly Pro

20 25

Lys Asp Gly Ser Gln Thr Glu Lys Thr Pro Ser Ala Asp Gln Asn Gln 35 40 45

Glu Gln Phe Glu Glu His Phe Val Ala Ser Ser Val Gly Glu Met Trp 50 55 60

Gln Val Val Asp Met Ala Gln Gln Glu Glu Asp Gln Ser Ser Lys Thr
65 70 75 80

Ala Ala Val His Lys His Ser Phe His Leu Ser Phe Cys Phe Ser Leu 85 90 95

Ala Ser Val Met Val Phe Ser Gly Gly Pro Leu Arg Arg Thr Phe Pro 100 100 105 110

Asn Ile Gln Leu Cys Phe Met Leu Thr His Xaa 115 120

<210> 155

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals stop translation

<400> 155

Met Lys Gln Phe Gly Phe Gly His Pro Ile Lys Leu Leu Lys Thr Lys 1 5 10 15

Leu Cys Arg Ile Val Phe Tyr Leu Val Phe Phe Val Trp Pro Gln Ser 20 25 30

Ser Val Ile Arg Glu Ala Thr Gln Thr Xaa 35 40

<210> 156

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (56)

<223> Xaa equals stop translation

<400> 156

Met Val Leu Ala Ala Pro Leu Val Ala Phe Pro Cys Ile Leu Leu Phe 1 5 10 15

Ala Phe Ser Pro Ser Ala Val Arg Asp His Val Gly Asp Ser Arg Ser

20 25 30

Asp Val Pro Ile Phe Ala Cys Leu Ala Leu Ala Ser Leu Ala Leu Gly

Ser Val Leu Leu Val Ala Phe Xaa

<210> 157

<211> 45

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (45)

<223> Xaa equals stop translation

<400> 157

Met Met Lys Met Val Leu Gly Leu Phe Phe Leu Met Asn Leu Leu Ser

Gly Lys Lys Ser Val Arg His His Ser Lys Asn Tyr Val Lys Lys Met 25

Gln Thr Phe Gln Phe Pro Arg Val Tyr Lys Leu Met Xaa 40

<210> 158

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (86)

<223> Xaa equals stop translation

Met Lys Lys Val Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val

Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser 25

Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr

Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe 55

Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro 75

Leu Pro Ser Glu Lys Xaa

```
<210> 159
  <211> 45
  <212> PRT
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (45)
  <223> Xaa equals stop translation
  <400> 159
 Met Ile Cys Leu Cys Ser Ile Lys Met Leu Leu Phe Cys Gln Leu
 Thr Phe Ala Leu Ile Thr Cys Ile Asn Leu Gln Ser Leu Tyr Leu Phe
                                   25
 Ser Tyr Gln Gln Ile Ile Gly Ile His Ser His Val Xaa
 <210> 160
 <211> 69
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (69)
 <223> Xaa equals stop translation
 <400> 160
Met Trp Leu Arg Gly Ile His Pro Phe Leu Trp Leu Ser Gly Ile His
. Ser Phe Pro Trp Leu Ser Gly Gly Pro Ser Leu Gly Thr Ser Ser Glu
             20
                                  25
Gln Pro Thr Ser Leu Glu Asp Gly Lys Leu Ile Cys Leu Phe Thr Asp
Phe Ser Gly Ser Ser Phe Gly Leu Phe Met Arg Glu Ala Ala Lys Asn
Ile Ser Gln Met Xaa
 65
<210> 161
<211> 53
<212> PRT
<213> Homo sapiens
<220>
```

<221> SITE <222> (53)

<223> Xaa equals stop translation

<400> 161

Met Leu Tyr Asp Ser Asn Leu Cys Ser Val Trp His Leu Tyr Leu Ile

Leu His Leu Cys Lys Thr Phe Val Tyr Cys Gly Cys Val His Ser Ser 25

Tyr Leu Ile Ser Gly Thr Val Asn Thr Gln Tyr Phe Ile Val Gln Thr

Val Leu Leu Phe Xaa 50

<210> 162

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (57)

<223> Xaa equals stop translation

<400> 162

Met Arg Val Lys Ile Ser Tyr Leu Met Ile Ala Leu Thr Val Val Gly

Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg His Glu 25

Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys Glu Glu

Ala Ala Met Lys Ala Lys Thr Glu Xaa 50

<210> 163

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (56)

<223> Xaa equals stop translation

<400> 163

Met Arg Glu Lys Thr Gly Ala Leu Pro Arg Cys Leu Gly Leu Leu Gly 10

Val Gly Leu Leu Trp Arg Trp Cys Gly Arg Arg Ala Arg Ala Gly Val

20 25 30

Gly Lys Ala Trp Ser Ala Thr Arg Ser Pro Ser Asp Ser Cys Phe Pro 35 40 45

Gly Val Ala Arg Val Gly Ile Xaa 50 55

<210> 164

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (48)

<223> Xaa equals stop translation

<400> 164

Met His Gly His Thr Ser Ser Leu Pro Pro Ser Leu Leu Ser Ser Leu 1 5 10 15

Pro Ser Gly Leu Leu Ala Leu Phe Val Phe Pro Phe Leu Ile Leu Leu 20 25 30

Leu His Ala Glu Asp Leu Pro Tyr Tyr Tyr Phe Gly Asn Ile Glu Xaa $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

<210> 165

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (130)

<223> Xaa equals stop translation

<400> 165

Met Ser Ala Ser Ser Leu His Arg Leu Pro Val Leu Met Ala Leu Phe

1 5 10 15

Pro Phe Gln Ala Ala Ala Ala Gly Ser Leu Gly Leu Gln Pro Pro Pro 20 25 30

Thr Pro Met Lys Gly Lys Pro Ser Ile Met Leu Pro Pro Gln Tyr Lys
35 40 45

Arg Arg Glu Gly Leu Lys Lys Lys Lys Lys Lys Ile Gln Lys Val Ala
50 55 60

Leu Val Ser Phe Gly Arg Ala Asp Ser Ile Val Gly Asp Gly Leu Pro

96

65 70 75 80

Thr Asn Gln Gly Asp Lys Cys Gln Arg Glu Arg Thr Met Pro Gly Ser 85 90 95

Lys His Ile Ser Pro Gln Thr Pro Gln Val Gly Lys Gln Ala Arg Gly 100 105 110

Ser Thr Asn Pro Ser Gly Arg Pro Gly Val Gln Met Leu Tyr Ser Ser 115 120 125

Ile Xaa 130

<210> 166

<211> 105

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (105)

<223> Xaa equals stop translation

<400> 166

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu 1 5 10

Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg

Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr 35 40 45

Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg 50 55 60

Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg
65 70 75 80

Tyr His Ser Gly Leu Trp Leu Gln Thr Leu Gln Lys Ile Thr Pro Phe
85 90 95

Leu Leu Leu Arg Cys Asn Gln Pro Xaa 100 105

<210> 167

<211> 77

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (77)

<223> Xaa equals stop translation

<400> 167

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser Val 1 5 10 15

Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Ala Pro Arg 20 25 30

Thr Ser Thr Cys Thr Arg Pro Ser Leu Gly Arg Thr Arg Gly Arg Arg 35 40 45

Cys Pro Arg Pro Gly Arg Thr Gly Gln Gly Ala His Gly Arg Leu Arg 50 55 60

Cys Arg Arg Val Ser Gly Gln Phe Leu Met Leu Ala Xaa 65 70 75

<210> 168

<211> 355

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (355)

<223> Xaa equals stop translation

<400> 168

Met Trp Arg Leu Trp Pro Gly Ser Pro Leu Val Pro Leu Ser Trp Leu

1 5 10 15

Trp Pro Ala Arg Ala Ala Phe Leu Ser Gly Pro Trp Thr Leu Pro Pro 20 25 30

Cys Leu Pro Asp Pro Leu Leu Ala Val Pro Lys Cys Cys Leu Thr Leu 35 40 45

Gly Ile His Leu Leu Pro Ala Trp Pro Gly Pro Pro Val Gly Gly Gly 50 55 60

Cys Ser Gln Leu His Arg Gly Cys Cys Tyr Pro Gly Met Gly Cys Leu
65 70 75

Asn Arg Asp Leu Cys Pro Pro Ser Leu Val Ser Arg Arg Trp Gly Asp

Gln Leu Leu Trp Ser Pro Asp Gly Ser Lys Ile Leu Ala Thr Thr Pro 100 105 110

Ser Ala Val Phe Arg Val Trp Glu Ala Gln Met Trp Thr Cys Glu Arg

Trp Pro Thr Leu Ser Gly Arg Cys Gln Thr Gly Cys Trp Ser Pro Asp 130 135 140

Gly Ser Arg Leu Leu Phe Thr Val Leu Gly Glu Pro Leu Ile Tyr Ser

145 150 155 160

Leu Ser Phe Pro Glu Arg Cys Gly Glu Gly Lys Gly Cys Val Gly Gly

Ala Lys Ser Ala Thr Ile Val Ala Asp Leu Ser Glu Thr Thr Ile Gln 185

Thr Pro Asp Gly Glu Glu Arg Leu Gly Gly Glu Ala His Ser Met Val

Trp Asp Pro Ser Gly Glu Arg Leu Ala Val Leu Met Lys Gly Lys Pro

Arg Val Gln Asp Gly Lys Pro Val Ile Leu Leu Phe Arg Thr Arg Asn

Ser Pro Val Phe Glu Leu Leu Pro Cys Gly Ile Ile Gln Gly Glu Pro 245 250

Gly Ala Gln Pro Gln Leu Ile Thr Phe His Leu Pro Ser Thr Lys Gly

Pro Cys Ser Val Trp Ala Gly Pro Gln Ala Glu Leu Pro Thr Ser Arg 280

Cys Thr Leu Ser Met Pro Ser Phe His Val Leu Ala Gln Cys Leu Gly 295

Gly Pro Arg Asn Pro Leu Leu Gly Val Glu Ala Leu Phe Met Thr Cys 315

Pro Ser Leu Leu Arg His Pro Gln Pro Leu Pro Leu Gly Thr Leu Ser 325

Gln Gly His His Leu Phe Cys Pro Thr Pro His Ile Pro Thr Ser Lys 345

Asn Lys Xaa 355

<210> 169

<211> 90

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (90)

<223> Xaa equals stop translation

<400> 169

Met Cys Val Cys Tyr Phe Leu Val Phe Leu Gln Ile Trp Ala Arg Leu 5

Ser His Leu Leu Val Trp Ile Tyr Pro Gly Ala Gly Leu Gln Pro Gly

30

20 25

Lys Gly His Pro Ala Gln Ser Leu Phe Pro His Glu His Cys His Leu 40

Met Pro Gln His Ser Leu Thr Leu Lys Ile Leu Glu Glu Lys Leu Gly 55

Gly Lys Gly Glu Ser Gly Ser Asn Phe Thr Phe Leu His Cys Lys Ile 70 75

Leu Ala Thr Ser Ala Leu Asn Phe Ser Xaa 85

<210> 170

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals stop translation

<400> 170

Met Val Leu Pro Phe Val Leu Leu Phe Arg Pro Asn Phe Ile Ser Val

Leu His Pro Leu Phe Tyr Ser His Cys Leu Phe Leu Tyr Leu Ile Ser 25

Pro Val His Ser Ser Ser Ile Ile Tyr Tyr Lys Pro Asp His Cys His 40

Tyr Thr Pro Phe Ile Pro Gly Leu Leu Gln Xaa 50 55

<210> 171

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (70)

<223> Xaa equals stop translation

Met Leu Leu Ser Lys Glu His Thr Ser Leu Gly Trp Leu Val Ile Phe

Leu Thr Leu Ala Ser Gln Leu Ile Ser Tyr Gly Ser Arg Thr Gly Asn 25

Ser Arg Cys Pro Pro Cys Leu Tyr Arg Thr Leu His Thr Val Ser Thr

Ser His Val Leu Ser Ser Leu Phe Val Ser Thr Phe Ser Gly Asp Glu 55

100

Leu Val Trp Thr Thr Xaa 65

35

<210> 172

<211> 79

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (79)

<223> Xaa equals stop translation

<400> 172

Met Val Leu Asp Phe Lys Arg Ala Gly Ser Phe Phe Leu Ser Phe Leu

Trp Thr Arg Glu Ala Phe Ala Phe Ile Phe Thr Leu Pro Leu Leu 20 25

Ser Leu Cys Arg Gly Lys Met Lys Asn Ser Pro Arg Ser Asp Leu Ser

Arg Leu Lys Lys Asn Val Phe Asn Ala Phe Leu Pro Cys Leu Val Pro 55

Arg Phe Ile Ser Asn Arg Gly Cys Pro Val Tyr Arg Ser Cys Xaa 70

<210> 173

<211> 174

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (150)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (152)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (174)

<223> Xaa equals stop translation

<400> 173

101

Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser 1 5 10 15

Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Asp Ile Thr Ala Ala 20 25 30

Ala Leu Ala Thr Gly Ala Cys Ile Val Glu Ser Ser Ala Ser Pro Ser 35 40 45

Ser Cys Ser Trp Ser Thr Ser Lys Gly Arg Gln Pro Pro Thr Ala Val 50 55 60

Pro Arg Ser Trp Cys Gly Trp Thr Ala Thr Phe Lys Gly Leu Lys Thr 65 70 75 80

Pro Ala Leu Lys Pro His His Leu Pro Arg Gly Tyr Pro Arg Pro Lys
85 90 95

Ser Gly Thr Pro Cys Pro Met Trp Pro Ser Gly Ser Leu Leu Ser Leu 100 105 110

Gly Gly Ile Cys Phe Arg Ser Pro Ala Pro Pro Cys Leu Leu Gln Ala 115 120 125

Pro Glu Thr Ser Ser Ser His Pro Trp Thr Leu Ser Leu Thr Leu Gln 130 135 140

Gly Ser Gly Ala Gly Ala Phe Glu Pro Gly Leu Ala Leu Xaa 165 170

<210> 174

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (64)

<223> Xaa equals stop translation

<400> 174

Met Phe Val Leu Trp Val Phe Lys Ile Thr Tyr Ile Tyr Ile Leu Phe 1 5 10 15

Ala Lys Asn Lys Ser Leu Ala Ser Cys Gln Met Ile Ala Lys Val Asp 20 25 30

Leu Thr Phe Phe Val Ile Met Tyr Ile Phe Ile His Thr Pro Asn Thr 35 40 45

Leu Ser Asp Phe Cys Tyr Phe Leu Gly Ser Thr Ala Leu Arg Leu Xaa 50 55 60

```
<210> 175
 <211> 43
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (43)
 <223> Xaa equals stop translation
 Met Ile Ser Ala Gln Ser Ser Ile Ser Trp Ala Leu Ile Phe Ile Met
 Ala Pro Ala Leu His Leu Val Leu Arg Phe Pro Ser Lys Phe Lys Pro
Glu Arg Lys Gly Glu Ala Arg Ser Pro Lys Xaa
<210> 176
<211> 114
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (114)
<223> Xaa equals stop translation
<400> 176
Met Trp Ile Ala Gly Pro Ser Trp Val Pro Leu Arg Tyr Val Val Trp
Leu Met His Leu Glu Arg Ile Cys Ala Leu His Asn Cys Arg Gly Asn
Met Leu Ser Trp Pro Leu Gln Ile Arg Val Ala Val Leu Gly Cys Cys
Thr Lys Thr Pro Ala Val Gly Phe Leu Gln Val Ala Gly Ser Pro His
Ser Cys Gln Asp Pro Gly Pro Cys Ser His Ser Ala Ala Ile Phe Pro
Pro Cys Glu Arg Gly Leu Cys Gly Asp Gly Pro Arg Cys Val Arg Gly
                 85
Cys Val His Cys His Arg Ser Leu Leu His Glu Pro Ala Trp Thr Gln
           100
                               105
```

```
Gly Xaa
```

```
<210> 177
  <211> 156
  <212> PRT
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (156)
  <223> Xaa equals stop translation
 <400> 177
 Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val Ser Leu
                                       10
 Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser Val Leu
 Gly Pro Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala Asp Leu
 Pro Cys His Leu Phe Pro Thr Met Ser Ala Glu Thr Met Glu Leu Lys
 Trp Val Ser Ser Ser Leu Arg Gln Val Val Asn Val Tyr Ala Asp Gly
                     70
                                          75
 Lys Glu Val Glu Asp Arg Gln Ser Ala Pro Tyr Arg Gly Arg Thr Ser
                  85
                                      90
 Ile Leu Arg Asp Gly Ile Thr Ala Gly Lys Ala Ala Leu Arg Ile His
Asn Val Thr Ala Ser Asp Ser Gly Lys Tyr Leu Cys Tyr Phe Gln Asp
        115
                             120
Gly Asp Phe Tyr Glu Lys Ala Leu Val Glu Leu Lys Val Ala Ala Leu
Gly Ser Asn Leu His Val Gly Ser Glu Gly Leu Xaa
145
                    150
<210> 178
<211> 89
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (89)
<223> Xaa equals stop translation
```

<400> 178

104

Met Trp Pro Ser Gln Val Pro Leu Leu Ala Phe Cys Phe Leu Leu Val 1 5 15

Lys Ser Thr Ser Asn Ile Asn Leu Pro Thr Pro Pro Pro Ser Ser Leu 20 25 30

Glu Asn Ser Ser Phe Val Val Ser Gln Arg Gly Asn Leu Ile Val Phe 35 40 45

Gly Gly Gln Lys Lys Ala Thr Phe Arg Tyr His Phe Tyr Leu Asp Arg 50 55 60

Val Asn Gly Tyr Leu Cys Asn Asn Xaa 85

<210> 179

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (197)

<223> Xaa equals stop translation

<400> 179

Met Ala Phe Arg Tyr Leu Ser Trp Ile Leu Phe Pro Leu Leu Gly Cys

1 5 10 15

Tyr Ala Val Tyr Ser Leu Leu Tyr Leu Glu His Lys Gly Trp Tyr Ser 20 25 30

Trp Val Leu Ser Met Leu Tyr Gly Phe Leu Leu Thr Phe Gly Phe Ile 35 40 45

Thr Met Thr Pro Gln Leu Phe Ile Asn Tyr Lys Leu Lys Ser Val Ala 50 55 60

His Leu Pro Trp Arg Met Leu Thr Tyr Lys Ala Leu Asn Thr Phe Ile 65 70 75 80

Asp Asp Leu Phe Ala Phe Val Ile Lys Met Pro Val Met Tyr Arg Ile

Gly Cys Leu Arg Asp Asp Val Val Phe Phe Ile Tyr Leu Tyr Gln Arg

Trp Ile Tyr Arg Val Asp Pro Thr Arg Val Asn Glu Phe Gly Met Ser 115 120 125

Gly Glu Asp Pro Thr Ala Ala Ala Pro Val Ala Glu Val Pro Thr Ala 130 135 140

105

Ala Gly Ala Leu Thr Pro Thr Pro Ala Pro Thr Thr Thr Thr Ala Thr 145 150 155 160

Arg Glu Glu Ala Ser Thr Ser Leu Pro Thr Lys Pro Thr Gln Gly Ala 165 170 175

Ser Ser Ala Ser Glu Pro Gln Glu Ala Pro Pro Lys Pro Ala Glu Asp 180 185 190

Lys Lys Lys Asp Xaa 195

<210> 180

<211> 129

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (129)

<223> Xaa equals stop translation

<400> 180

Met Tyr Glu Cys Phe Leu Ser Leu Ser Leu Leu Lys Ser Cys Lys Ala 1 5 10 15

Val Ser Gly Leu Met Cys Leu Leu Leu Pro Arg Leu Gly Leu Leu Leu 20 25 30

Leu Leu Pro Ser Glu Arg Cys Phe Cys Trp Ile Pro Val Tyr Ser Leu 35 40 45

Ile Thr Cys Leu Ala Glu Cys Ser Val Val Leu Arg Asp Pro Gly Phe 50 55 60

Ala Gly Ala Phe Gln Val His Arg Arg Gln Ala Cys Phe Ser Thr Leu 65 70 75 80

Arg Trp Ser Cys Leu Leu Leu Trp Trp Val Ser Arg Val Ser Ala Gly 85 90 95

Arg Pro Leu Ile Gly Ser Pro His Met Met Ala Pro Ser Thr Phe Cys

Pro Thr Val Arg Gly Pro Gly Thr Cys Ala Ser Ser Asp Pro Asp Gly 115 120 125

Xaa

<210> 181

<211> 155

<212> PRT

<213> Homo sapiens

<220>
<221> SITE
<222> (155)
<223> Xaa e

WO 99/31117

<223> Xaa equals stop translation

<400> 181

Met Pro Ala Glu Lys Arg Ile Phe Gly Ala Val Leu Leu Phe Ser Trp

1 5 10 15

Thr Val Tyr Leu Trp Glu Thr Phe Leu Ala Gln Arg Gln Arg Ile
20 25 30

Tyr Lys Thr Thr Thr His Val Pro Pro Glu Leu Gly Gln Ile Met Asp 35 40 45

Ser Glu Thr Phe Glu Lys Ser Arg Leu Tyr Gln Leu Asp Lys Ser Thr 50 60

Phe Ser Phe Trp Ser Gly Leu Tyr Ser Glu Thr Glu Gly Thr Leu Asn 65 70 75 80

Leu Leu Phe Gly Gly Ile Pro Tyr Leu Trp Arg Leu Ser Gly Arg Phe 85 90 95

Cys Gly Tyr Ala Gly Phe Gly Pro Glu Tyr Glu Ile Thr Gln Ser Leu 100 105 110

Val Phe Leu Leu Leu Ala Thr Leu Phe Ser Ala Leu Thr Gly Val Pro 115 120 125

Trp Ser Leu Tyr Asn Thr Phe Val Ile Lys Lys Thr Trp Leu Gln Ser 130 135 140

<210> 182

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (107)

<223> Xaa equals stop translation

<400> 182

Met Ser Leu Ser Trp Met Val His Leu Leu Gly Leu Pro Asn Gly Thr 1 5 10 15

Val Trp Tyr Leu Pro Phe Val Cys Phe Thr Arg Gly Ser Pro Met Gly
20 25 30

Gly Gly Ser Gly Gln Trp Arg Trp Asp Arg Lys Phe Ser Lys Thr Leu $35 \hspace{1cm} 40 \hspace{1cm} 45$

107

Leu Gly Asn Leu Phe Val Ala Phe Lys Glu Met Cys Gly Glu Asp Ile 50 60

Trp Met Leu Ala Ala Ile Leu Glu Leu Arg Thr Gln Glu Trp Trp Lys
65 70 75 80

Gly Arg Arg Asn Arg Val Phe Val Ala Val Val Lys Leu Leu Lys Phe
85 90 95

Pro Ser Cys Gln Ala Ser Cys Tyr Met Arg Xaa 100 105

<210> 183

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (48)

<223> Xaa equals stop translation

<400> 183

Met Ile Asn Glu Trp Cys Phe Lys Leu Leu Ser Leu Trp Ser Phe Ala 1 5 10 15

Tyr Ser Asn Cys Lys Leu Ile His Lys Cys Lys Phe Val Phe Leu Lys 20 25 30

Lys Lys Lys Thr Gly Lys Glu Val Ser Val Lys Gly Ser Lys Leu Xaa 35 40 45

<210> 184

<211> 127

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (127)

<223> Xaa equals stop translation

<400> 184

Met Trp Leu Gly Ser Trp Leu Thr Ser Leu Leu Leu Ser Pro Tyr Gly

1 5 10 15

Ser Gly Trp Glu Lys Val Pro Cys Cys Val Thr Gly His Leu Arg Ser 20 25 30

Cys Ser Cys Cys Leu Leu Gly Leu Ala Gly Val Gln Ser Asp His Phe 35 40 45

Ser Glu Gly Phe Phe Ser Glu Tyr Ser Ser Asp Val Leu Pro Trp Gly 50 55 60

Arg Arg Ser Phe Leu Pro Gln Gly Asp Ala Ser Leu Leu Ala Cys Glu 65 70 75 80

Cys Phe Leu His Leu Gln Val Val Trp Gly Gln Phe Cys Leu Leu Glu 85 90 95

Ala Trp Ala Gly Phe Thr Glu Gly Ser Met Pro Ala Pro Ser Cys Arg

Val His Phe Trp Cys Arg Val Asn Thr Cys Pro Phe Met Ser Xaa 115 120 125

<210> 185

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (87)

<223> Xaa equals stop translation

<400> 185

Met Leu Cys Gly Tyr Val Ile Asn Asn Ile Trp Leu Ile Phe Thr Tyr

1 5 10 15

Phe Ile Cys Ile Tyr Ile Ser Arg Ser Tyr Ile Tyr Ile Thr Gln Glu
20 25 30

Thr Gln Val Ile Tyr Ile Cys Gln Glu Met Tyr Asp Tyr Phe Gly Glu
35 40 45

Asn Gly Pro Lys Cys Glu Lys Asp Ile Lys Lys Thr Lys Lys Thr Lys 50 55 60

Lys Lys His Tyr Phe Pro Leu Arg Asn Ile Leu Tyr Ile Ser Lys Glu 65 70 75 80

Glu Lys Leu Lys Asp Ile Xaa 85

<210> 186

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (58)

<223> Xaa equals stop translation

<400> 186

Met Ile Val Ser Tyr Arg Ile Val Ser Leu Pro Ser Ser Val Leu Cys 5

Leu Phe Ile Pro Pro Phe Leu Leu Ile Phe Tyr Cys Leu His Ser Phe

Val Phe Ser Gln Met Leu Tyr Ser Trp Asn Tyr His Val Thr Phe Gln 40

Met Ala Phe Ser Leu Ile Ile Cys Val Xaa 55

<210> 187

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (69)

<223> Xaa equals stop translation

<400> 187

Met Val Ala Ser Gln Ala Trp Trp Leu Ser Asn Leu Trp His Leu Trp

Glu Val Gly Ser Ala Gln Gly Leu Pro Leu Asp Pro Pro Ala Leu Ala 25

Pro Tyr Leu Pro Trp Ala Leu Arg Trp Pro Cys Phe Ser Gly Phe Ala 40

Ser Leu Ala Gly Ala Leu Val Leu Ala His Ser Leu Pro Thr Ala Trp

Pro Gly Ser Ser Xaa 65

<210> 188

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (48)

<223> Xaa equals stop translation

Met Tyr Leu Phe Leu Cys Cys Phe Ile Ser Glu His Cys Ala Gln 5

His Ser Phe Pro His Thr Cys Pro Asn Trp Lys Thr Arg Val Leu Ser 20 25

Phe Pro Leu His Pro Cys Pro His Leu Ile His Pro Asn Asn Thr Xaa 35 40 45

<210> 189 <211> 51 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (5) <223> Xaa equals any of the naturally occurring L-amino acids <220> <221> SITE <222> (51) <223> Xaa equals stop translation <400> 189 Met Leu Ser Ser Xaa Tyr Val Pro Met Cys Gln His Phe Ile Tyr Pro Val Leu Trp Val Leu Val His Phe Phe Ser Phe Ile Gln Ile Gln Lys 25 Asn Thr Asp Gly Ser Asn Val Lys Leu Thr Arg Asn Pro Gly Thr Phe Ile Ser Xaa 50 <210> 190 <211> 56 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (56) <223> Xaa equals stop translation <400> 190 Met Ala Val Arg Val Leu Trp Gly Gly Leu Ser Leu Leu Arg Val Leu Trp Cys Leu Leu Pro Gln Thr Gly Tyr Val His Pro Asp Glu Phe Phe 25 Gln Ser Pro Glu Val Met Ala Gly Lys Thr Pro His Val Trp Leu Arg 35 40

SUBSTITUTE SHEET (RULE 26)

Gln Ala Ala Glu Ser Ala Xaa

50 55

<210> 191

<211> 127

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (127)

<223> Xaa equals stop translation

<400> 191

Met Cys Ser Ser Phe Pro Arg Met Ala Leu Cys Ala Leu Trp Met Trp 1 5 10 15

Pro Ser Val Lys Ser Ser Val Pro Leu Pro Leu Arg Glu Pro Phe Leu 20 25 30

Trp Arg Ser Pro Gly Ser Gln Cys Leu Leu Cys Leu Gln Thr Ile His 35 40 45

Val Ser Cys Ser Glu Ala Cys Pro Leu Leu Glu Asn Ile Ser Lys Asn 50 55 60

Cys Thr Ile Pro Gln Arg Asp Leu Asp Asn Met Ala Phe Pro Gln Ala 65 70 75 80

Leu Pro Leu Glu Lys Arg Cys Glu Arg Phe Leu Gln Lys Ser Tyr Arg

Lys Leu Glu Lys Asn Pro Glu Lys Glu Glu Glu His Trp Ala Arg Leu 100 105 110

Gln Arg Tyr Ser Leu Ser Leu Gln Arg Glu Asn Phe Lys Lys Xaa 115 120 125

<210> 192

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (70)

<223> Xaa equals stop translation

<400> 192

Met Pro Phe Gln Leu Pro Leu Gln Leu Leu Leu Leu Arg Leu Ile Cys

1 5 10 15

Glu Phe Phe Leu Ala Pro Ala Leu Asn Cys Asn Leu Thr Gly Thr Val 20 25 30

Ile Phe Phe Thr Leu Met Ile Ser Leu Gln Leu Met Ile Phe Phe Thr

PCT/US98/27059 WO 99/31117 112

35 40 45

Leu Gln Phe Ala Asp Gly Phe Gln Ile Gly Val Asp Leu Gln Leu Ser 60

Glu Leu Asn Ile Leu Xaa

<210> 193

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (71)

<223> Xaa equals stop translation

<400> 193

Met Ile Ser Gly Val Leu Ile Phe Asn Leu Ile Ala Ser Ser Trp Val 10

Leu Cys Phe Pro Leu Cys Asp Leu Ser Cys Gln Lys Thr Leu Arg Ile

Phe Phe Ala Ser Phe Phe His Ala Val Cys Val His Val Ser Cys Thr 35 40

Ser Trp Gln Pro Leu Val Leu Phe Ile Lys Trp Trp Val Val Gly Cys

Ser Pro Ala Val Ser Leu Xaa

<210> 194

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (130)

<223> Xaa equals stop translation

<400> 194

Met His Val Leu Pro Leu Leu Leu Ser Leu Leu Leu Leu Leu Leu Leu 5

Leu Ser Ala Ser Phe Val Thr Phe Ser Thr Pro Thr Ser Ser Arg Asn 25

Ser Ser Cys Pro Asp Cys Glu Ser Leu Asn Thr Gly Leu Pro Ser Leu 40

Met Met Phe Gly Gly Ser Leu Leu Lys Trp Val Gln Asn Thr His Gly

50 55 60

Val Glu Ser Leu Leu Ser Ser Ala Lys Val Arg Leu Leu Pro Pro Ala 75

Leu Gly Val Leu Phe Pro Arg Leu His Pro Gly Thr Leu Thr Leu Val

Phe Leu Leu Ile Pro Phe Leu Thr Val Ser Ser Thr Ser Asp Val

Leu Ser Ser Leu Glu Ser Pro Lys Leu Ser Val Thr Ile Phe His Tyr 115 120

Cys Xaa 130

<210> 195 <211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (55)

<223> Xaa equals stop translation

<400> 195

Met Pro Trp Ile Leu Met Leu Leu Phe Thr Met Gly Gln Gly Val Val

Ile Leu Ala Phe Arg Ser Cys Leu Glu Ala Glu Val Arg Gly Val Pro 20

Gly Arg Gly Asn Arg Ser Gly Val Lys Thr Val Val Glu Ala Pro Ala 40

Val Phe Ala Lys Arg Pro Xaa 50

<210> 196

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (80)

<223> Xaa equals stop translation

<400> 196

Met Ala Ala Phe Phe Ala Leu Ala Ala Leu Val Gln Val Val Tyr Thr 10

Ile Pro Ala Val Leu Thr Leu Leu Val Gly Leu Asn Pro Glu Val Thr

20 25 30

Gly Asn Val Ile Trp Lys Ser Ile Ser Ala Ile His Ile Leu Phe Cys 40

Thr Val Trp Ala Val Gly Leu Ala Ser Tyr Leu Leu His Arg Thr Gln

Gln Asn Ile Leu His Glu Glu Glu Gly Arg Ser Cys Leu Val Trp Xaa

<210> 197

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals stop translation

<400> 197

Met Lys His Met Asn Thr Leu Pro Ile Phe Ser Ser Leu Ile Ser Phe 10

Leu Pro Ala Val Ser Ala Gly Arg Ser Ala Ile Thr Thr Leu Cys Asn

Ile Thr Glu Gln Leu Glu Val Leu Gly Xaa

<210> 198

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (197)

<223> Xaa equals stop translation

<400> 198

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala 35 40

Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn

60

115 55

Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val 65 70 75

Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln

Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Val 100 105 110

Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg 115 120 125

Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu 130 135 140

Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn 145 150 150 155 160

Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp
165 170 175

Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Arg Trp 180 185 185

Thr Gly Val Thr Xaa 195

<210> 199

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (124)

<223> Xaa equals stop translation

<400> 199

Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
1 5 10 15

Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly 20 25 30

His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys 35 40 45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg 50 55 60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
65 70 75 80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val

116

85 90 9

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr 100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser Xaa 115 120

<210> 200

<211> 549

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (132)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (398)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 200

Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys

1 5 10 15

Leu Leu Ser Ala Leu Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro
20 25 30

Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu 35 40 45

Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu 50 55 60

Ser Phe Val Arg Ser Gly Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu 65 70 75 80

Phe Thr Pro Ser Leu Gln Leu Leu Leu Phe Thr Ser Asn Ser Phe Asp 85 90 95

Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu 100 105 110

Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg 115 120 125

Gly Leu Lys Xaa Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln
130 135 140

Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val 145 150 155 160

Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu 165 170 175

- Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys 180 185 190
- Glu Gly Pro Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser 195 200 205
- Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu 210 215 220
- Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu 225 230 235 240
- Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu 245 250 255
- Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Gly 260 265 270
- Thr Ser Thr Val Val Cys Lys Pro Ile Val Ile Glu Thr Gln Leu Tyr 275 280 285
- Val Ile Val Ala Gln Leu Phe Gly Gly Ser His Ile Tyr Lys Arg Asp 290 295 300
- Ser Phe Ala Asn Lys Phe Ile Lys Ile Gln Asp Ile Glu Ile Leu Lys 305 310 315 320
- Ile Arg Lys Pro Asn Asp Ile Glu Thr Phe Lys Ile Glu Asn Asn Trp 325 330 335
- Tyr Phe Val Val Ala Asp Ser Ser Lys Ala Gly Phe Thr Thr Ile Tyr 340 345 350
- Lys Trp Asn Gly Asn Gly Phe Tyr Ser His Gln Ser Leu His Ala Trp 355 360 365
- Tyr Arg Asp Thr Asp Val Glu Tyr Leu Glu Ile Val Arg Thr Pro Gln . 370 380
- Thr Leu Arg Thr Pro His Leu Ile Leu Ser Ser Ser Ser Xaa Arg Pro 385 390 395 400
- Val Ile Tyr Gln Trp Asn Lys Ala Thr Gln Leu Phe Thr Asn Gln Thr 405 410 415
- Asp Ile Pro Asn Met Glu Asp Val Tyr Ala Val Lys His Phe Ser Val 420 425 430
- Lys Gly Asp Val Tyr Ile Cys Leu Thr Arg Phe Ile Gly Asp Ser Lys 435 440 445
- Val Met Lys Trp Gly Gly Ser Ser Phe Gln Asp Ile Gln Arg Met Pro 450 455 460
- Ser Arg Gly Ser Met Val Phe Gln Pro Leu Gln Ile Asn Asn Tyr Gln 465 470 475 480

PCT/US98/27059

Tyr Ala Ile Leu Gly Ser Asp Tyr Ser Phe Thr Gln Val Tyr Asn Trp
485 490 495

Asp Ala Glu Lys Ala Lys Phe Val Lys Phe Gln Glu Leu Asn Val Gln 500 510

Ala Pro Arg Ser Phe Thr His Val Ser Ile Asn Lys Arg Asn Phe Leu 515 520 525

Phe Ala Ser Ser Phe Lys Gly Asn Thr Gln Ile Tyr Lys His Val Ile 530 535 540

Val Asp Leu Ser Ala 545

<210> 201

<211> 488

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (344)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (416)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (429)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (430)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 201

Met Ile Leu Ser Leu Leu Phe Ser Leu Gly Gly Pro Leu Gly Trp Gly 1 5 10 15

Leu Leu Gly Ala Trp Ala Gln Ala Ser Ser Thr Ser Leu Ser Asp Leu 20 25 30

Gln Ser Ser Arg Thr Pro Gly Val Trp Lys Ala Glu Ala Glu Asp Thr
35

Ser Lys Asp Pro Val Gly Arg Asn Trp Cys Pro Tyr Pro Met Ser Lys
50 55 60

Leu Val Thr Leu Leu Ala Leu Cys Lys Thr Glu Lys Phe Leu Ile His
65 70 75 80

WO 99/31117

- Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Lys Val Lys 85 90 95
- Val Met Tyr Arg Met Ala His Lys Pro Val Tyr Gln Val Lys Gln Lys 100 105 110
- Val Leu Thr Ser Leu Ala Trp Arg Cys Cys Pro Gly Tyr Thr Gly Pro 115 120 125
- Asn Cys Glu His His Asp Ser Met Ala Ile Pro Glu Pro Ala Asp Pro 130 135 140
- Gly Asp Ser His Gln Glu Pro Gln Asp Gly Pro Val Ser Phe Lys Pro 145 150 155 160
- Gly His Leu Ala Ala Val Ile Asn Glu Val Glu Val Gln Gln Glu Gln
 165 170 175
- Gln Glu His Leu Leu Gly Asp Leu Gln Asn Asp Val His Arg Val Ala 180 185 190
- Asp Ser Leu Pro Gly Leu Trp Lys Ala Leu Pro Gly Asn Leu Thr Ala 195 200 205
- Ala Val Met Glu Ala Asn Gln Thr Gly His Glu Phe Pro Asp Arg Ser 210 215 220
- Leu Glu Gln Val Leu Leu Pro His Val Asp Thr Phe Leu Gln Val His 225 235 240
- Phe Ser Pro Ile Trp Arg Ser Phe Asn Gln Ser Leu His Ser Leu Thr 245 250 255
- Gln Ala Ile Arg Asn Leu Ser Leu Asp Val Glu Ala Asn Arg Gln Ala 260 265 270
- Ile Ser Arg Val Gln Asp Ser Ala Val Ala Arg Ala Asp Phe Gln Glu 275 280 285
- Leu Gly Ala Lys Phe Glu Ala Lys Val Gln Glu Asn Thr Gln Arg Val 290 295 300
- Gly Gln Leu Arg Gln Asp Val Glu Glu Arg Leu His Ala Gln His Phe 305 310 315 320
- Thr Leu His Arg Ser Ile Ser Glu Leu Gln Ala Asp Val Asp Thr Lys 325 330 335
- Leu Lys Arg Leu His Lys Ala Xaa Glu Ala Pro Gly Thr Asn Gly Ser 340 345 350
- Leu Val Leu Ala Thr Pro Gly Ala Gly Ala Arg Pro Glu Pro Asp Ser 355 360 365
- Leu Gln Ala Arg Leu Gly Gln Leu Gln Arg Asn Leu Ser Glu Leu His 370 375 380

Met Thr Thr Ala Arg Glu Glu Glu Leu Gln Tyr Thr Leu Glu Asp 385 390 395 400

Met Arg Ala Thr Leu Thr Arg His Val Asp Glu Ile Lys Glu Leu Xaa 405 410 415

Ser Glu Ser Asp Glu Thr Phe Asp Gln Ile Ser Lys Xaa Xaa Arg Gln 420 425 430

Val Glu Glu Leu Gln Val Asn His Thr Ala Leu Arg Glu Leu Arg Val 435 440 445

Ile Leu Met Glu Lys Ser Leu Ile Met Glu Glu Asn Lys Glu Glu Val 450 455 460

Glu Arg Gln Leu Leu Glu Leu Asn Leu Thr Leu Gln His Leu Gln Gly 465 470 475 480

Gly Met Pro Thr Ser Ser Ser Thr 485

<210> 202

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (86)

<223> Xaa equals stop translation

<400> 202

Met Ala His Gly Pro Gln Ser Leu Trp Ser Leu Gly Phe Thr Val Thr 1 5 10 15

Leu Thr Phe Glu Leu Pro Val Gly Cys Val Leu Gly Arg Ile Cys His 20 25 30

Pro Ile Gln Ala Cys Asn Thr Gly Leu Met Thr Pro Thr Pro Gln Gly 35 40 45

Pro Cys Arg Thr Glu Met Met Ser Asn Asp Lys Pro Trp Leu Pro Ala 50 60

Asn Ala Pro Ala His Ile Ser Leu Pro Gly Ala Arg Leu Thr Ser Thr 65 70 75 80

Cys Ala Pro Gly Leu Xaa

<210> 203

<211> 400

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (400)

<223> Xaa equals stop translation

<400> 203

Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe 1 5 10 15

Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser
20 25 30

Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala 35 40 45

Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr
50 55 60

Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp
65 70 75 80

Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly
85 90 95

Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp 100 105 110

Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala 115 120 125

Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu 130 135 140

Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala 145 150 155 160

Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile 165 170 175

Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser 180 185 190

Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp 195 200 205

Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Gly Ala Phe 210 215 220

Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys 225 230 235 240

His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp
245 250 255

Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser 260 265 270

Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala 275 280 285

Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr 290 295 300

Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg 305 310 315 320

Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met 325 330 335

Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys 340 345 350

Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser 355 360 365

Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu 370 380

Glu Leu Thr Thr Ser Ser Ser His Gly Pro Pro Pro Thr Ala Arg Xaa 385 390 395 400

<210> 204

<211> 195

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (195)

<223> Xaa equals stop translation

<400> 204

Met Ser Thr Ala Phe Cys Pro Ile His Ser Ser Leu Gly Ser Met Val 1 5 10 15

Met Cys Leu Cys Ile Leu Ser Pro Leu Cys Ile Ala Ser Lys Ser Leu 20 25 30

Arg Val Cys Thr Lys Ser Tyr Met Glu Gly His Gly Lys Thr Arg Val
35 40 45

Pro Val Val Leu Val Gly Asn Lys Ala Asp Leu Ser Pro Glu Arg Glu 50 55 60

Val Gln Ala Val Glu Gly Lys Lys Leu Ala Glu Ser Trp Gly Ala Thr 65 70 75 80

Phe Met Glu Ser Ser Ala Arg Glu Asn Gln Leu Thr Gln Gly Ile Phe 85 90 95

Thr Lys Val Ile Gln Glu Ile Ala Arg Val Gly Glu Phe Leu Trp Ala 105 Arg Ala Ser Leu Pro Ser His Val Ser Pro Trp Val Trp Gly Asn Cys 120 Leu Ala Ser Ala Pro Gly Thr Cys His Val Pro Val Gly Gly Arg Ser 135 Ser Gly Leu His Gly Tyr Gly Cys Gln Leu Cys Ser Trp Pro Leu Asp 155 Thr Gln Cys Gly Ile Leu Met Phe Ala His Phe Pro Gln Ala Pro Val 170 Ala Trp Met Ser Met Phe Thr Lys Gly Gln Gly Pro Leu Met Asp Thr 180 Gly Leu Xaa 195 <210> 205 <211> 57 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (57) <223> Xaa equals stop translation <400> 205 Met Pro Leu Glu Glu Ser Phe Glu Ile Val Leu Lys Leu Val Pro Leu Leu Gly Leu Glu Leu Phe Phe Phe Leu Phe Ile Ile Asn Gly Tyr Ile 20 25 Asn Val Tyr Cys Pro Ser Gln Tyr Phe Ile Tyr Ala Lys Asp Ser Leu Ala Gly Leu Ala Leu Ile Pro Gln Xaa 50 <210> 206 <211> 73 <212> PRT <213> Homo sapiens <220>

<221> SITE <222> (73)

<223> Xaa equals stop translation

<400> 206

Met Ile Val Ile Tyr Leu Thr Leu Thr Trp Thr Phe Leu Ile Asn Leu 1 5 10 15

Leu Ala Cys Pro Leu Tyr His Leu Pro Gln Met Gln Lys Lys Ala Lys 20 25 30

Pro Glu Thr Lys Lys Ala Lys Pro Glu Thr Lys Glu Thr Ile Gln Arg 35 40 45

Gln Arg Asn Leu Phe Leu Val Leu Leu Lys Gln Leu Ala Gly Lys Lys 50 55 60

Cys Ser Ala Leu Phe Leu Ile Val Xaa 65 70

<210> 207

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (85)

<223> Xaa equals stop translation

<400> 207

Met Val Trp Cys Gln Cys Leu Cys Pro Leu Cys Ala Cys Trp Glu Glu 1 5 10 15

Ala Gln Ala Leu Trp Trp Pro Pro Leu Cys Thr Trp Pro Gly Glu Ala
20 25 30

Arg Gly Ser Gly Ala Ser Leu Arg Leu Arg Pro Pro Leu Gln Asn Lys 35 40 45

Leu Ser Pro Gly Val Cys Leu Ser Leu Phe Leu Ser Pro Glu Arg Asn 50 55 60

Ala Gly Val Pro Glu Ala Ser Leu Gln Thr Lys His Pro Cys Thr Ser 65 70 75 80

Tyr Gly Ser Gly Xaa

<210> 208

<211> 195

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (195)

<223> Xaa equals stop translation

<400> 208

Met Trp Val Ser Leu Tyr Phe Gly Ile Leu Gly Leu Cys Ser Val Ile 1 5 10 15

Thr Gly Gly Cys Ile Ile Phe Leu His Trp Arg Lys Asn Leu Arg Arg
20 25 30

Glu Glu His Ala Gln Gln Trp Val Glu Val Met Arg Ala Ala Thr Phe
35 40 45

Thr Tyr Ser Pro Leu Leu Tyr Trp Ile Asn Lys Arg Arg Tyr Gly
50 55 60

Met Asn Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr 65 70 75 80

Glu Thr Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro 85 90 95

Glu Gly Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala 100 105 110

Pro Ala Pro Leu Gln Pro Ala Leu Gln Leu Ala Pro Gln Gln Pro Gln 115 120 125

Ala Arg Ser Pro Phe Pro Leu Pro Ile Phe Gln Glu Val Pro Phe Ala 130 135 140

Pro Pro Leu Cys Asn Leu Pro Pro Leu Leu Asn His Ser Val Ser Tyr 145 150 155 160

Pro Leu Ala Thr Cys Pro Glu Arg Asn Val Leu Phe His Ser Leu Leu 165 170 175

Asn Leu Ala Gln Glu Asp His Ser Phe Asn Ala Lys Pro Phe Pro Ser 180 185 190

Glu Leu Xaa 195

<210> 209

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals stop translation

<400> 209

Met Leu Gln Arg Gly Gln His Leu Tyr Leu Val Val Phe Leu Met Val 1 5 10 15

Ser Phe Ile Pro Leu Leu Asn Pro Lys Gln Asp Leu Lys Lys Leu Lys 20 25 30

Lys Asn Arg Thr Val Arg Asn His Phe Xaa 35 40

<210> 210

<211> 282

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (282)

<223> Xaa equals stop translation

<400> 210

Met Ser Ile Leu Thr Met Ile Ser Ser Trp Pro Phe Ser Arg Val Val
1 5 10 15

Arg Phe Trp Phe Leu His Gln Met Val Leu Asp Leu Cys Leu Gly Gln 20 25 30

Gly Val Pro Gln Gln Asn Leu Gly Lys Pro Lys Gly Lys Lys Leu 35 40 45

Ser Ser Val Arg Gln Lys Phe Asp His Arg Phe Gln Pro Gln Asn Pro 50 55 60

Leu Ser Gly Ala Gln Gln Phe Val Ala Lys Asp Pro Gln Asp Asp Asp 65 70 75 80

Asp Leu Lys Leu Cys Ser His Thr Met Met Leu Pro Thr Arg Gly Gln 85 90 95

Leu Glu Gly Arg Met Ile Val Thr Ala Tyr Glu His Gly Leu Asp Asn 100 105 110

Val Thr Glu Glu Ala Val Ser Ala Val Val Tyr Ala Val Glu Asn His 115 120 125

Leu Lys Asp Ile Leu Thr Ser Val Val Ser Arg Arg Lys Ala Tyr Arg 130 135 140

Leu Arg Asp Gly His Phe Lys Tyr Ala Phe Gly Ser Asn Val Thr Pro 145 150 155 160

Gln Pro Tyr Leu Lys Asn Ser Val Val Ala Tyr Asn Asn Leu Ile Glu 165 170 175

Ser Pro Pro Ala Phe Thr Ala Pro Cys Ala Gly Gln Asn Pro Ala Ser 180 185 190

His Pro Pro Pro Asp Asp Ala Glu Gln Gln Ala Ala Leu Leu Leu Ala 195 200 205

Cys Ser Gly Asp Thr Leu Pro Ala Ser Leu Pro Pro Val Asn Met Tyr 210 215 220

127

Asp Leu Phe Glu Ala Leu Gln Val His Arg Glu Val Ile Pro Thr His 225 230 235 240

Thr Val Tyr Ala Leu Asn Ile Glu Arg Ile Ile Thr Lys Leu Trp His 245 250 255

Pro Asn His Glu Glu Leu Gln Gln Asp Lys Val His Arg Gln Arg Leu 260 265 270

Ala Ala Lys Glu Gly Leu Leu Cys Xaa 275 280

<210> 211

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (48)

<223> Xaa equals stop translation

<400> 211

Met Pro Lys Thr Cys Leu Pro Ile Leu Cys Leu Pro Leu Thr Gln Ala 1 5 10 15

Val Val Leu Ala Gln Leu Asn Asn Phe Ser Ser Leu Asn Ile Phe Ile
20 25 30

Phe Lys Ile Lys Asn Lys Met Tyr Tyr Ile Trp Ile Tyr Asp Lys Xaa 35 40 45

<210> 212

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals stop translation

<400> 212

Met Trp Pro Cys Cys Leu Asp Ser Leu Leu Phe Gly Phe Trp Leu Trp

1 5 10 15

Ala Gln Gly Ile Thr Leu Leu Ser Glu Asp Ser Ile Arg Ile Val Cys
20 25 30

Ser Ser Cys Glu Pro Glu Val Leu His Val Pro Thr Pro Val Tyr Arg 35 40 45

```
Pro Cys Pro Ser His Ser Pro Leu Thr Phe Xaa
    50
                        55
<210> 213
<211> 43
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (43)
<223> Xaa equals stop translation
<400> 213
Met Ala Leu Gln Ser Ile Pro Ser Phe Thr Leu Leu Ile Ser Phe Phe
                                     10
Leu Ser Thr Gln Cys Leu Arg Cys Val Tyr Asn Tyr Glu Cys Ile Leu
Phe Met Ala Phe Asn Cys Arg Met Val Phe Xaa
                             40
<210> 214
<211> 53
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (53)
<223> Xaa equals stop translation
<400> 214
Met Pro Ala Val Ser Ala Phe Phe Ser Leu Ala Ala Leu Ala Glu Val
Ala Ala Met Glu Asn Val His Arg Gly Gln Arg Ser Thr Pro Leu Thr
His Asp Gly Gln Pro Lys Glu Met Pro Gln Ala Pro Val Leu Ile Ser
         35
                             40
Cys Ala Asp Gln Xaa
     50
<210> 215
<211> 68
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
```

<222> (68)

<223> Xaa equals stop translation

<400> 215

Met Cys Thr Gln Ile Leu Val Phe Met Leu Leu Ile Lys Cys Ile Phe 5

Ser Ile Asn Thr His Pro Ile Met Pro Tyr Leu Tyr Met Lys Asn Lys 25

Val Thr Met Leu Tyr Cys Tyr Val Leu Lys Phe Lys Ser Leu Phe Glu 40

Lys Pro Ser Asn Trp Cys Phe His Tyr Ile Met Ile His Leu Asp Lys

Thr Pro Asn Xaa 65

<210> 216

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (57)

<223> Xaa equals stop translation

<400> 216

Met Leu Phe Val Ser Leu Leu Val Met Trp Asn Leu Phe Leu Ser Ser 10

Asp Phe Leu Phe Leu Trp Ser Val Leu Gly Tyr Tyr Met Lys Val Arg 20 30

Leu Pro Gln Ser Pro Arg Glu Ala His Cys Val Leu Leu Ile Asp Leu

Lys Met Ile Glu Ser Leu Gly Gly Xaa

<210> 217

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (56)

<223> Xaa equals stop translation

<400> 217

Met Glu Gln Leu Leu Ala Ala Val Val Phe Phe Ser Ile Phe Phe Leu 10

Asn Leu Leu Ala Leu Lys Met Asn Lys Val Tyr Arg Cys Ile Cys Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Leu Phe Ser Lys Asn Met His Thr Asn Val Cys Phe Tyr Lys Ser Asn 35 40 45

Thr His Val Ile Ile Cys Met Xaa 50 55

<210> 218

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (58)

<223> Xaa equals stop translation

<400> 218

Met Cys Trp Lys Pro Lys Cys Ile Leu Leu Leu Ser Phe Val Phe Gln
1 5 10 15

Cys Val Ala Ser Ser Thr Phe Asp Pro Leu Gly Ser Glu Arg Pro Trp
20 25 30

Ser Gln Pro Gln Cys Pro Ile Ser Phe Pro Leu Leu Ile Thr Gly Cys 35 40 45

Cys Trp Phe Ser Met Ser Arg Val Ser Xaa 50 55

<210> 219

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals stop translation

<400> 219

Met Arg Thr Phe Leu Thr Phe Val Ile Leu Lys Val Ile Leu Ile Phe 1 5 10 15

Leu Ser Ser Cys Ala Ser Phe Thr Arg Asn Leu Leu Thr Trp Pro Asn 20 25 30

Asp Val Ser Thr Glu Gln Phe Glu Thr Arg Pro Phe Gly Ser Glu Leu
35 40

Leu Gln Thr Val Ile Asn Val Ser Arg Thr Xaa 50 55

```
<210> 220
 <211> 45
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (45)
 <223> Xaa equals stop translation
 <400> 220
 Met Arg Phe Phe Gln Ala Tyr Ser Gln Ile Cys Val Gln Asn Phe
 Leu Thr Phe Leu Cys Ile Ile Ile Glu Phe Ile Ala Ala Asp Phe
                                  25
Tyr Asn Asp Ser Cys Cys His Val Ser Leu Asn Asn Xaa
                              40
<210> 221
<211> 45
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (41)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (45)
<223> Xaa equals stop translation
Met Ile Leu Phe Asp Leu Thr Phe Phe Leu Phe Ala Pro Arg Ile Leu
Ala Ser Gly Ala Cys Ser Cys Ser Ile Tyr Pro Lys Ile Thr Leu Pro
Thr Lys Tyr Phe Ala Phe Ile Ile Xaa Thr Ser Phe Xaa
                             40
<210> 222
<211> 52
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (52)
```

<223> Xaa equals stop translation

<400> 222

Met Asp Gly Leu Ile Met Cys Leu Ile Ile Phe Gln Ile Val Asn Phe 1 5 10 15

Trp Leu Pro Cys Ile Ile Leu Leu Gly Ile Leu Asn Pro Thr Tyr Lys
20 25 30

Asn Tyr Val Met Val Ser Thr Lys Cys Trp Met Lys Arg Thr Tyr Glu 35 40 45

His Met Ser Xaa 50

<210> 223

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (73)

<223> Xaa equals stop translation

<400> 223

Met Thr Phe Leu Phe Phe Phe Leu Phe Ser Arg Ile Leu Cys Ile Lys
1 5 10 15

Asn Leu Asp Leu Leu Thr Trp Lys Arg Ser Asn Pro Val Ile Ala Lys
20 25 30

His Leu Tyr Cys Arg Gly His Ile Thr Lys Lys Ser Lys Gly Pro Ala 35 40 45

Gln Trp Thr Ile Tyr Phe Ser Asp Val Gln Tyr Lys Ile Ser Leu Pro 50 55 60

Leu Lys Thr Leu Glu Ser Pro Phe Xaa 65 70

<210> 224

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (71)

<223> Xaa equals stop translation

<400> 224

Met Leu Phe Trp Lys Phe Gly Ser Phe Leu Phe Phe Cys Leu Pro Leu 1 5 10 15

133

Thr Leu Phe Cys Ile Leu Asn Glu Arg Gly Ile Met His Leu Glu Gly 20 25 30

Gly Thr Leu Leu Asn Ser Leu Ser His Val Arg His Tyr Leu Arg Leu 35 40 45

Arg Leu Ser Cys Phe Glu Lys Ile Pro Leu His Arg Ser Ile Phe Ile 50 55 60

Phe Leu Leu Leu Leu Xaa 65 70

<210> 225

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (58)

<223> Xaa equals stop translation

<400> 225

Met Ala Gly Cys Cys Leu Lys Leu Phe Gly Val Leu Ser Leu Cys Phe 1 5 10 15

Leu Cys Gly Leu Ile Ser Ile Glu Arg Val Ile Cys Asn Pro Val Ser 20 25 30

Ala Asp Phe Gln Val Ser Thr Phe Cys Gln Arg His Cys Leu Leu Arg 35 40 45

Ser Lys Val Met Phe Pro Ile Arg Gly Xaa 50 55

<210> 226

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals stop translation

<400> 226

Met Arg Ile Ser Arg Cys Asn Ile Ser Leu Glu Ile Val Ser Pro Ser 1 5 10 15

Ile Leu Leu Thr Phe Leu Asp Leu Ile Ile Leu Leu Trp Ala Leu Ala
20 25 30

Ser Cys Tyr Arg Arg Phe Thr Ser Phe Pro Ala Leu Asn Leu Pro Asp 35 40 45

PCT/US98/27059

Val Asn Ser Thr Leu His Tyr Leu Gln Gln Xaa 50 55 <210> 227 <211> 43 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (43) <223> Xaa equals stop translation Met Val Ala Pro Leu His Leu Phe Ile Pro Phe Ser Trp Leu Val Arg 5 10 Thr Ile Gly Gln Leu Leu Ser Pro Val Gly Lys Ala Leu Ser His Arg Ser Asn Gln Met Met Pro Arg Ser Trp Gly Xaa 40 <210> 228 <211> 41 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (41) <223> Xaa equals stop translation <400> 228 Met Arg Thr Ser Leu Phe Phe Phe Phe Phe Lys Asn Ile Leu Val Leu 1 . 5 10 Cys Gly Thr Leu Leu Ile Ser Arg Ser Ser His Ser Gln Ser Ala Pro Arg Gly Cys Trp Trp Pro His Lys Xaa <210> 229 <211> 42 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (42) <223> Xaa equals stop translation <400> 229

135

Met Leu Trp Lys Tyr Phe Leu Ser Leu Phe Leu Pro Trp Tyr Leu Tyr 1 5 10 15

Cys Phe Phe Asn Asn Asn Ile Met Phe Tyr Ser Leu His Ser Val Pro 20 25 30

Met Phe Ile Gln Pro Phe Leu Leu Trp Xaa 35 40

<210> 230

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (165)

<223> Xaa equals stop translation

<400> 230

Met Ser Thr Arg Arg Leu Gly Val Ala Val Ala Val Leu Gly Gly Phe $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Leu Tyr Ala Val Gly Gly Ser Asp Gly Thr Ser Pro Leu Asn Thr Val

Glu Arg Tyr Asn Pro Gln Glu Asn Arg Trp His Thr Ile Ala Pro Met 35 40 45

Gly Thr Arg Arg Lys His Leu Gly Cys Ala Val Tyr Gln Asp Met Ile 50 55 60

Tyr Ala Val Gly Gly Arg Asp Asp Thr Thr Glu Leu Ser Ser Ala Glu 65 70 75 80

Arg Tyr Asn Pro Arg Thr Asn Gln Trp Ser Pro Val Val Ala Met Thr 85 90 95

Ser Arg Arg Ser Gly Val Gly Leu Ala Val Val Asn Gly Gln Leu Met 100 105 110

Ala Val Gly Gly Phe Asp Gly Thr Thr Tyr Leu Lys Thr Ile Glu Val 115 120 125

Phe Asp Pro Asp Ala Asn Thr Trp Arg Leu Tyr Gly Gly Met Asn Tyr 130 135 140

Arg Arg Leu Gly Gly Gly Val Gly Val Ile Lys Met Thr His Cys Glu
145 150 155 160

Ser His Ile Trp Xaa 165

<210> 231 <211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (52)

<223> Xaa equals stop translation

<400> 231

Met Ala Cys Leu Ile Arg Phe Pro Ala Ile Gly Ser Leu Pro Tyr Ser 1 5 10 15

Thr Trp Pro Phe Phe Phe Ile Phe Leu Phe Phe Ser Cys Leu Thr 20 25 30

Phe Ile Pro Phe Ser Pro Leu Ser Ser Phe Cys Glu Pro Tyr Pro Arg 35 40 45

Lys Glu Pro Xaa 50

<210> 232

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (130)

<223> Xaa equals stop translation

<400> 232

Met Phe Leu Leu Asn Phe Arg Tyr Ile Met Arg Phe Phe Phe Trp Pro 1 5 10 15

Met Leu Gln Ala Lys Leu Met Ser Phe His Phe Leu Lys Pro Ile Ile 20 25 30

Phe Met Asn Ser Leu Ile Leu Cys Leu Lys Gln Ser Cys Ser Cys Glu 35 40

Val Glu Ile Ser Leu Leu Pro Leu Ser Gln Gln Thr His Arg Thr Asp 50 55 60

Leu Gly Phe Ser His Ser Gly Ser Gln Asn Glu Pro Phe Leu Asn Leu 65 70 75 80

Asp Lys Arg Ala Ala Glu Ala His Cys Ala Val Met Val Leu Cys Leu 85 90 95

Leu Gly Arg Asp Leu Lys Ala Arg Arg Ser Arg Glu Gly Pro Ala Leu 100 105 110

Cys Ser Ser Gln Val Val Ile Cys Ile Leu Lys Leu Ala Arg Lys Arg 115 120 125

```
Phe Xaa
    130
 <210> 233
 <211> 55
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (55)
 <223> Xaa equals stop translation
 <400> 233
 Met Glu Phe Lys Leu Val Arg Lys Ile Gln Ile Ala Ile Leu Ile Phe
 Tyr Leu Tyr Leu Val Ala Val Ala Phe Lys Asn Lys Phe Ser Tyr Lys
                                  25
Ser Phe Gln Phe Phe Gly Leu Glu Ser Ile Phe Gln Asn Lys Lys Leu
Lys Lys Glu Tyr Leu Met Xaa
     50
<210> 234
<211> 363
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (307)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (363)
<223> Xaa equals stop translation
<400> 234
Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
             20
                                 25
Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
                             40
Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
     50
                                             60
Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
```

80

70

65

Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr

Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln
100 105 110

Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp 115 120 125

Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu 130 135 140

His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe 145 150 155 160

Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr 165 170 175

Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu 180 185 190

Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Thr Asp Gln Leu Gly
195 200 205

Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly 210 215 220

Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro 225 230 235 240

Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro 245 250 255

Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly 260 265 270

Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala 275 280 285

Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp
290 295 300

Ser Gln Xaa Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly 305 310 315 320

Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu 325 330 335

Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly 340 345 350

Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu Xaa 355 360

```
<210> 235
<211> 29
 <212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (29)
<223> Xaa equals stop translation
Met Cys Met Cys Val Leu Leu Cys Val Phe Leu Ile Cys Lys Tyr Ser
Lys Ser Phe Leu Ile Leu Arg Leu Lys Phe Ser Cys Xaa
             20
<210> 236
<211> 67
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (67)
<223> Xaa equals stop translation
<400> 236
Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
Leu Leu Ser Ala Leu Leu Thr Glu Gly Lys Lys Pro Ala Asn Gln
             20
                                  25
Asn Ala Leu Pro Cys Val Leu Val Pro Lys Ile Met Leu Tyr Val Arg
Met Pro Asp Pro Phe His Ala Pro Phe Leu Leu Met Leu Ser His Tyr
Pro Leu Xaa
 65
<210> 237
<211> 114
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (114)
<223> Xaa equals stop translation
<400> 237
Met Ile Leu Ser Leu Leu Phe Ser Leu Gly Gly Pro Leu Gly Trp Gly
```

5 10

Leu Leu Gly Ala Trp Ala Gln Ala Ser Ser Thr Ser Leu Ser Asp Leu

Gln Ser Ser Arg Thr Pro Gly Val Trp Lys Ala Glu Ala Glu Asp Thr

Ser Lys Asp Pro Val Gly Arg Asn Trp Cys Pro Tyr Pro Met Ser Lys 50

Leu Val Thr Leu Leu Ala Leu Cys Lys Thr Glu Lys Phe Leu Ile His

Ser Gln Gln Pro Cys Pro Gln Glu Leu Gln Thr Ala Arg Lys Ser Lys 90

Ser Cys Thr Ala Trp Pro Thr Ser Gln Cys Thr Arg Ser Ser Arg Arg

Cys Xaa

1

<210> 238

<211> 106

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (106)

<223> Xaa equals stop translation

<400> 238

Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe

Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser 20

Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala

Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr 55

Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp 70

Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Leu Arg Gly Arg Cys His

His Thr Ala Gly Thr Met Gly Ser Cys Xaa

PCT/US98/27059

141

```
<210> 239
```

<211> 15

<212> PRT

<213> Homo sapiens

<400> 239

Gly Leu Gly Pro Ala Gln Val Ala Leu Ser Leu Gln Gly Pro Ala 1 5 10 15

<210> 240

<211> 82

<212> PRT

<213> Homo sapiens

<400> 240

Ser Ser Trp Met Ala Gly Thr Gln Pro Arg Thr Ser Trp Trp Glu Met

1 5 10 15

Ser Ser Ala Lys Pro Cys Pro Thr Gly Thr Leu Arg Ser Asn Thr Ser 20 25 30

Ser His Pro Gln Cys Thr Gly Pro Pro Thr Thr His Pro Met Leu Val 35 40 45

Gly Glu Asp Met Ser Cys Pro Glu Pro Gln Cys Gly Ala Ser Arg Leu 50 55 60

Ser Trp Lys Met Leu Asn Ser Ser Pro Leu Met Met Ser Leu Trp Val 65 70 75 80

Cys Ala

<210> 241

<211> 23

<212> PRT

<213> Homo sapiens

<400> 241

Gln Pro Arg Thr Ser Trp Trp Glu Met Ser Ser Ala Lys Pro Cys Pro 1 5 10 ... 15

Thr Gly Thr Leu Arg Ser Asn

<210> 242

<211> 23

<212> PRT

<213> Homo sapiens

<400> 242

Met Ser Cys Pro Glu Pro Gln Cys Gly Ala Ser Arg Leu Ser Trp Lys $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

```
Met Leu Asn Ser Ser Pro Leu
20
```

<210> 243

<211> 98

<212> PRT

<213> Homo sapiens

<400> 243

Trp Val Ala Leu Tyr Ile Glu Gly Gly Met Lys Tyr Leu Thr Leu Val 1 5 10 15

Phe Leu Leu Gly Arg Ala Trp Arg Met Thr Ser Pro Thr Arg Arg Ser 20 25 30

Trp Ala Gly Ser Gln Pro Ser Arg Asn Ser Asn Thr Leu Gly Thr Trp

45

Thr Lys Thr Ser Ser Ser Pro Phe Ser Met Lys Trp Ala Trp Gly Gln
50 55 60

Ala Ala Thr Thr Gln Arg Cys Arg Cys Ser Ser Leu Ser Val Arg Leu 65 70 75 80

Lys Lys Ser Ser Val Lys Ser His Trp Arg Met Ser Ser Asn Ser Leu 85 90 95

Leu Ser

<210> 244

<211> 20

<212> PRT

<213> Homo sapiens

<400> 244

Gly Gly Met Lys Tyr Leu Thr Leu Val Phe Leu Leu Gly Arg Ala Trp

1 5 10 15

Arg Met Thr Ser

20

<210> 245

<211> 25

<212> PRT

<213> Homo sapiens

<400> 245

Ser Gln Pro Ser Arg Asn Ser Asn Thr Leu Gly Thr Trp Thr Lys Thr 1 5 10 15

Ser Ser Ser Pro Phe Ser Met Lys Trp
20 25

```
<210> 246
 <211> 26
 <212> PRT
 <213> Homo sapiens
<400> 246
Thr Thr Gln Arg Cys Arg Cys Ser Ser Leu Ser Val Arg Leu Lys Lys
Ser Ser Val Lys Ser His Trp Arg Met Ser
             20
<210> 247
<211> 223
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (14)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (113)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (117)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (121)
```

		144													
<22	3> X	aa e	qual:	s an	y of	the	nat	ural	ly c	ccur	ring	L-a	mino	aci	.ds
<22	0>														
<22	1> S	ITE													
<22	2> (122)													
<22	3> X	aa e	qual	s an	y of	the	nat	ural	ly c	ccur	ring	L-a	mino	aci	ds
<22	0>														
<22	1> S	ITE													
<22	2> (125)													
<22	3> X	aa e	qual	s an	y of	the	nat	ural	ly c	ccur	ring	L-a	mino	aci	ds
<22	n>														
	1> S	TTE													
		129)													
			qual	s an	v of	the	nati	ural	lv o	ccur	ring	L-a	mino	aci	ds
			-	•	•										
<22	0>														
	l> S														
	2> (_		_			_	_						
<22.	3> X	aa e	qual:	s any	y of	the	nat	ural	ly o	ccur	ring	L-a	mino	aci	ds
<400)> 2	47													
Ala	Ser	Thr	Leu	Ala	Gln	Thr	Thr	Gly	Thr	Cys	Lys	Xaa	Xaa	Xaa	Ser
1				5					10					15	
Ser	Δτα	Ara	Ala	7~~	802	λ ~ α	ωρ.~	Cln	λ ~~ <i>~</i>	Vaa	Dho	C1 ~	T ou	7	Dwo
Ser	мц	Ary	20	Arg	261	Arg	THE	25	Arg	лаа	Pne	GIN	30 Leu	Arg	PIO
			20					23					30		
Asp	Lys	Arg	Ser	Ala	Pro	Ser	Leu	Leu	Gln	Phe	Ile	Gln	Ala	Gln	Glu
		35					40					45			
Glu		Ser	Lys	Glu	Asn		Gly	Arg	Gln	Leu	Ala	Ala	Arg	Glu	Ala
	50					55					60				
17-1	T 011	λ 1 -	T 0	G1	01	C	m ⊾	01	T	m\	01	D	57_ T	ml	Q1
65	rea	Ald	Leu	GIU		ser	Thr	GIN	ьeu		GIĀ	Pro	vaı	Thr	
03					70					75					80
Val	Ala	Ala	Ser	Lvs	Thr	His	Cvs	Ser	Glv	Met	Ala	Leu	Thr	Ala	Ser
				85					90					95	
Pro	Val	Pro	Val	Leu	Gly	Ala	Ala	Pro	Ala	Lys	Xaa	Pro	Thr	Gln	Asn
			100					105					110		
Xaa	Pro		Gln	Xaa	Gly	Arg	Ala	Xaa	Xaa	Lys	Val	Xaa	Thr	Ser	Trp
		115					120					125			
V	V				_			1		_			_		
лаа		vaı	Ala	unr	гля		Leu	His	GLY	Leu		Val	Ser	Thr	His
	130					135					140				
I,en	ദ്രാ	Lve	Arg	Lara	Low	c^~	G1	λ~~	C~~	П⊷∽	T 0	D~~	C1	D	^ ו ג
145	U-y	y.s	n. y	пλг	150	261	GIĀ	vī ā	ser.	155	ьeu	LTO	отЪ	PIO	160
										100					100
Leu	His	Ala	Thr	Pro	Ser	Gln	Ser	His	Thr	Gln	Thr	Glv	Ser	Gln	Ile
				165					170			2	-	175	
									-					_	

SUBSTITUTE SHEET (RULE 26)

Val His Pro Pro Gln Gly Glu Val Arg Glu Val Gly Arg Gly Arg Gly

145 180 185 190 Gln Pro Pro Ala Gln Pro Val His Ala His Pro Ser Gln Gln His Pro Ser Pro Ala His Leu Ala Gly Leu Ser Leu Trp Thr Gly Thr Ala 215

<210> 248 <211> 140 <212> PRT <213> Homo sapiens <220>

<221> SITE <222> (12)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE <222> (59)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (60)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (80)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (82)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 248

Ala Met Leu Glu Thr Trp Arg Pro Gly Pro Ser Xaa Gly Glu Leu Ala

Thr Asn Ser Gly Gln Arg Ala Ser Gln Asp Ser Gln His Ser Pro Pro 20

His Val Arg Ala His Leu Leu Ile Ser Pro Leu Pro Ala Phe Pro Ser

Met Gly Gly Pro Ala Gly Arg Ser Ala Pro Xaa Xaa Leu Thr Glu Thr 55

Lys Ser Glu Leu Gln Arg Leu Arg Arg Arg Gln Ala Arg Ala Ser Xaa 65 70

Ser Xaa Pro Ala Gly Glu Pro Gly Ala Gly His Ser Asp Ser Phe Asn 85 90

Cys Val Pro Thr Asn Gly Gln Pro Leu Arg Ser Cys Ser Leu Ser Lys 100 105 110

Leu Arg Arg Ser Phe Leu Lys Arg Thr Gln Gly Asp Ser Trp Leu Pro 115 120 125

Glu Lys Gln Ser Trp Leu Trp Lys Ala Pro Pro Ser 130 135 140

<210> 249 .

<211> 122

<212> PRT

<213> Homo sapiens

<400> 249

Ser His Gln Ser His Leu Ile Asn Pro Ala Ser Ser Ala Lys Gly Ser 1 5 10 15

Trp Ala Gln Leu Lys Ala Gln Pro Pro Ala His Val Leu Gly Gly Thr
20 25 30

Gly Gln Glu Gly Pro Pro Pro Thr Ala Asp Gln Pro Glu Ser Pro Gly 35 40 45

Trp Asp Pro Ser Ser Phe Thr Asn Gly Ser Ser Gly Pro Arg Ala Leu 50 55 60

Pro Thr Ser Val His Pro Thr Leu Gln Gln Gly Ala Pro Cys Arg Arg 65 70 75 80

Asn Trp Ala Pro Cys Arg Gly Leu Val Glu Thr Arg Met Leu Arg Arg 85 90 95

Gln Leu Pro His Gly Thr Ser Lys Arg Asp Leu Gly Trp Ala Ser Leu 100 105 110

Gln Arg Gly Ser Pro Gln Glu Thr Pro Gln 115

<210> 250

<211> 35

<212> PRT

<213> Homo sapiens

<400> 250

Arg Pro Asp Lys Arg Ser Ala Pro Ser Leu Leu Gln Phe Ile Gln Ala 1 5 10 15

Gln Glu Glu Leu Ser Lys Glu Asn Thr Gly Arg Gln Leu Ala Ala Arg 20 25 30

Glu Ala Val

35

```
<210> 251
 <211> 33
 <212> PRT
 <213> Homo sapiens
 <400> 251
 Ala Thr Pro Ser Gln Ser His Thr Gln Thr Gly Ser Gln Ile Val His
 Pro Pro Gln Gly Glu Val Arg Glu Val Gly Arg Gly Arg Gly Gln Pro
                                  25
 Pro
 <210> 252
 <211> 29
 <212> PRT
 <213> Homo sapiens
Gln Asp Ser Gln His Ser Pro Pro His Val Arg Ala His Leu Leu Ile
         - 5
Ser Pro Leu Pro Ala Phe Pro Ser Met Gly Gly Pro Ala
             20
<210> 253
<211> 28
<212> PRT
<213> Homo sapiens
<400> 253
Asp Ser Phe Asn Cys Val Pro Thr Asn Gly Gln Pro Leu Arg Ser Cys
Ser Leu Ser Lys Leu Arg Arg Ser Phe Leu Lys Arg
             20
<210> 254
<211> 25
<212> PRT
<213> Homo sapiens
<400> 254
Lys Gly Ser Trp Ala Gln Leu Lys Ala Gln Pro Pro Ala His Val Leu
 1
Gly Gly Thr Gly Gln Glu Gly Pro Pro
```

SUBSTITUTE SHEET (RULE 26)

<210> 255

PCT/US98/27059

148

```
<211> 26
<212> PRT
<213> Homo sapiens
<400> 255
Ala Pro Ser Leu Leu Gln Phe Ile Gln Ala Gln Glu Glu Leu Ser Lys
Glu Asn Thr Gly Arg Gln Leu Ala Ala Arg
             20
<210> 256
<211> 6
<212> PRT
<213> Homo sapiens
<400> 256
Lys Pro Ser His Gln Pro
 1
                 5
<210> 257
<211> 21
<212> PRT
<213> Homo sapiens
<400> 257
Cys Ser Tyr Arg Pro Gln Phe Pro Val Asp Pro Arg Val Arg Ala Thr
                5
                                     10
Cys Ile Val Phe Asn
             20
<210> 258
<211> 128
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (46)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (60)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (66)
<223> Xaa equals any of the naturally occurring L-amino acids
<400> 258
Gly Thr Glu Asn Leu Leu Ala Pro Glu Arg Thr Ile Leu Ser Arg Ala
```

149

5 10 15

Gln Met Gly Lys Cys Met Ala Thr Pro Ala Pro Cys Val Arg Ser Ser 20 25 30

Ser Lys Gln Lys Lys Lys Lys Arg Lys Arg Lys Val Xaa Gln Glu 35 40 45

Thr Lys Asp Asn Leu Arg Val Gln Leu Pro Leu Xaa Ser Cys Val Val 50 55 60

Asn Xaa Ala Asn Pro Gly Lys Thr Asp Gly Phe Phe Ala Pro Glu Arg 65 70 75 80

Met Thr Pro Ser Arg Ala Gln Met Glu Lys Cys Met Ala Thr Pro Ala 85 90 95

Pro Cys Val Arg Pro Ser Phe Asn Lys Lys Lys Glu Gln Glu Gln Arg

Leu Lys Glu Lys Leu Gln Arg Lys Ser Ala Val Asn Phe Gly Thr Lys
115 120 125

<210> 259

<211> 26

1

<212> PRT

<213> Homo sapiens

<400> 259

Leu Leu Ala Pro Glu Arg Thr Ile Leu Ser Arg Ala Gln Met Gly Lys

1 5 10 15

Cys Met Ala Thr Pro Ala Pro Cys Val Arg 20 25

<210> 260

<211> 24

<212> PRT

<213> Homo sapiens

<400> 260

Pro Gly Lys Thr Asp Gly Phe Phe Ala Pro Glu Arg Met Thr Pro Ser 1 5 10 15

Arg Ala Gln Met Glu Lys Cys Met 20

<210> 261

<211> 17

<212> PRT

<213> Homo sapiens

<400> 261

```
Glu Gln Arg Leu Lys Glu Lys Leu Gln Arg Lys Ser Ala Val Asn Phe
                   5
                                      10
Gly
<210> 262
<211> 186
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (68)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (69)
<223> Xaa equals any of the naturally occurring L-amino acids
<400> 262
Lys Thr Leu Leu Glu Asn Phe Ser Thr Gln Gly Thr Phe Val Ala Met
His Pro Ala Val Arg Ala Thr Asp Trp Ile Thr Leu Pro Cys Thr Lys
Lys Pro Ser Ile Ser His Leu Phe Phe Xaa Phe Leu Ala Lys Ile Leu
         35
                              4 C
Phe Ser Ile Ser Ser Asn Ser Ser Phe Thr Leu Ser Leu Gly Ile Phe
                          55
Ser Phe Phe Xaa Xaa Gln Leu Ser Thr His Cys Thr Leu Ile Ala Met
Arg Leu Pro Ile Arg Thr Lys Asn Arg Ile Ile Phe Pro Cys Ala Ser
                 85
Lys Ser Ser Ile Ser Asn Lys Gly Pro Lys Ser Thr Ala Tyr Ile Leu
Leu Trp Ile Thr Ala Leu Thr Phe Pro Phe Thr Phe Tyr Thr Asn Leu
                            120
                                                 125
Gly Pro Gly Phe Arg Ile Leu Ser Thr Gln Cys Thr Ser Val Val Ile
    130
                        135
```

Cys Phe Pro Ile Cys Ala Thr Asn Ser Phe Ile Ile Arg Thr Asp 145 150

Lys Ile Pro Ile Ser Phe Ser Phe Phe Lys Ile Ile Thr Ile Gln Leu 165 170

Cys Trp Gly Ser Ser Leu Gly Ser Ser Cys

<210> 263

<211> 22

<212> PRT

<213> Homo sapiens

<400> 263

Met His Pro Ala Val Arg Ala Thr Asp Trp Ile Thr Leu Pro Cys Thr 10

Lys Lys Pro Ser Ile Ser 20

<210> 264

<211> 17

<212> PRT

<213> Homo sapiens

<400> 264

Leu Ile Ala Met Arg Leu Pro Ile Arg Thr Lys Asn Arg Ile Ile Phe 5

Pro

<210> 265

<211> 26

<212> PRT

<213> Homo sapiens

<400> 265

Ser Ser Ile Ser Asn Lys Gly Pro Lys Ser Thr Ala Tyr Ile Leu Leu 5

Trp Ile Thr Ala Leu Thr Phe Pro Phe Thr 20

<210> 266

<211> 23

<212> PRT

<213> Homo sapiens

<400> 266

Ile Ile Ile Arg Thr Asp Lys Ile Pro Ile Ser Phe Ser Phe Phe Lys 5 10

```
Ile Ile Thr Ile Gln Leu Cys
<210> 267
<211> 165
<212> PRT
<213> Homo sapiens
```

<220> <221> SITE <222> (147)

<223> Xaa equals any of the naturally occurring L-amino acids <220>

<221> SITE

<222> (153)

<223> Xaa equals any of the naturally occurring L-amino acids

Asn Asp Gly Gln Cys Leu Ala Tyr Asn Thr Thr His Tyr Arg Glu Arg

Ala Met Thr Ser His Ala Arg Val Ser Leu Gly Pro Ser Arg Asp Pro

Lys Phe Glu His Thr Gly Thr His Gly Thr Leu Val Ser Met His Phe

Ala Ile Trp Ala Thr Asp Arg Ile Met Leu Pro Gly Ala Tyr Lys Cys

Ser Ile Pro His Leu Val Pro Lys Phe Thr Ala Asp Phe Leu Cys Ser

Phe Ser Phe Ser Leu Cys Ser Cys Ser Phe Phe Leu Leu Lys Glu Gly

Leu Thr His Gly Ala Gly Val Ala Met His Phe Ser Ile Trp Ala Leu

Asp Gly Val Ile Leu Ser Gly Ala Lys Lys Pro Ser Val Phe Pro Gly

Phe Ala Xaa Phe Thr Thr Gln Leu Xaa Lys Gly Ser Cys Thr Leu Arg Leu Ser Phe Val Ser 165

<210> 268 <211> 22

```
WO 99/31117
               <212> PRT
               <213> Homo sapiens
                                                    153
                                                                             PCT/US98/27059
              <400> 268
              Cys Leu Ala Tyr Asn Thr Thr His Tyr Arg Glu Arg Ala Met Thr Ser
             His Ala Arg Val Ser Leu
            <210> 269
            <211> 31
            <212> PRT
           <213> Homo sapiens
           <400> 269
          Gly Thr Leu Val Ser Met His Phe Ala Ile Trp Ala Thr Asp Arg Ile
         Met Leu Pro Gly Ala Tyr Lys Cys Ser Ile Pro His Leu Val Pro
        <210> 270
        <211> 24
        <212> PRT
        <213> Homo sapiens
       <220>
       <221> SITE
       <222> (18)
      <223> Xaa equals any of the naturally occurring L-amino acids
      <220>
     <221> SITE
     <222> (24)
     <223> Xaa equals any of the naturally occurring L-amino acids
    <400> 270
    Gly Val Ile Leu Ser Gly Ala Lys Lys Pro Ser Val Phe Pro Gly Phe
   Ala Xaa Phe Thr Thr Gln Leu Xaa
  <210> 271
  <211> 141
 <212> PRT
 <213> Homo sapiens
 <220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids
```

```
154
 <220>
 <221> SITE
 <222> (38)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (44)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (57)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (58)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <400> 271
 Lys Lys Ala Ser His Met Glu Gln Val Leu Pro Cys Ile Phe Pro Ser
  1
 Gly Pro Trp Met Gly Ser Phe Ser Leu Xaa Gln Lys Ser Arg Pro Phe
                                  25
 Phe Leu Asp Leu Arg Xaa Ser Leu His Asn Ser Xaa Lys Glu Ala Val
Leu Leu Asp Cys Leu Leu Phe Leu Xaa Xaa Pro Ser Phe Phe Phe Phe
             55
                                              60
Ser Ser Ser Ser Ala Trp Lys Lys Thr Ser His Met Glu Gln Val Leu
Pro Cys Thr Phe Pro Ser Gly Pro Trp Ile Gly Leu Phe Ser Leu Val
                 85
                                     90
Gln Ala Ser Phe Pro Phe Leu Thr Ser Phe Arg Tyr Ser Leu Gln Ser
            100
                                105
Ser Ala Tyr Glu Val Ala Phe Pro Asp Ser Leu Leu Phe Leu Ala Arg
                            120
Ala Ser Ala Phe Phe Phe Ser Ser Phe Ser Ala Trp Lys
    130
                      135
<210> 272
<211> 28
<212> PRT
<213> Homo sapiens
```

<220>

<221> SITE <222> (15)

<223> Xaa equals any of the naturally occurring L-amino acids <220> <221> SITE <222> (27) <223> Xaa equals any of the naturally occurring L-amino acids Cys Ile Phe Pro Ser Gly Pro Trp Met Gly Ser Phe Ser Leu Xaa Gln Lys Ser Arg Pro Phe Phe Leu Asp Leu Arg Xaa Ser 20 <210> 273 <211> 28 <212> PRT <213> Homo sapiens <400> 273 Trp Ile Gly Leu Phe Ser Leu Val Gln Ala Ser Phe Pro Phe Leu Thr Ser Phe Arg Tyr Ser Leu Gln Ser Ser Ala Tyr Glu 20 <210> 274 <211> 79 <212> PRT <213> Homo sapiens <400> 274 Asn Ser Ala Val Asn Ile Lys Ile Arg Gln Arg Met Glu Tyr Phe Ser 5 Val Pro Glu Lys Met Thr Leu Phe Val Val Gln Met Gly Lys Cys Met Ala Thr Cys Val Pro Cys Val Lys Pro Thr Ser Lys Gln Lys Met Lys 40 Lys Arg Lys Arg Leu Lys His Glu Leu Glu Thr Lys Glu Asn Leu Glu 50 Lys Gln Pro His Met Gln Ser Phe Ala Val Asn Ile Glu Ser Leu 65 70 <210> 275 <211> 23 <212> PRT <213> Homo sapiens <400> 275 Ile Lys Ile Arg Gln Arg Met Glu Tyr Phe Ser Val Pro Glu Lys Met

156

1 5 10 15

Thr Leu Phe Val Val Gln Met 20

<210> 276

<211> 25

<212> PRT

<213> Homo sapiens

<400> 276

Val Lys Pro Thr Ser Lys Gln Lys Met Lys Lys Arg Lys Arg Leu Lys

1 5 10 15

His Glu Leu Glu Thr Lys Glu Asn Leu 20 25

<210> 277

<211> 63

<212> PRT

<213> Homo sapiens

<400> 277

Pro Arg Val Arg Gly Thr Val Val Arg Leu Arg Gln His Arg Pro Ser 1 5 10 15

Ala Tyr Ile Leu Val Ser Thr Val Leu Thr Leu Met Val Pro Trp His
20 25 30

Ser Leu Asp Pro Asp Ser Ala Leu Ala Asp Ala Phe Tyr Gln Arg Gly 35 40

Tyr Arg Trp Ala Gly Phe Ile Val Ala Ala Gly Ser Ile Cys Ala 50 55 60

<210> 278

<211> 25

<212> PRT

<213> Homo sapiens

<400> 278

Thr Val Val Arg Leu Arg Gln His Arg Pro Ser Ala Tyr Ile Leu Val 1 5 10 15

Ser Thr Val Leu Thr Leu Met Val Pro 20 25

<210> 279

<211> 26

<212> PRT

<213> Homo sapiens

<400> 279

157

Trp His Ser Leu Asp Pro Asp Ser Ala Leu Ala Asp Ala Phe Tyr Gln
1 5 10 15

Arg Gly Tyr Arg Trp Ala Gly Phe Ile Val 20 25

<210> 280

<211> 101

<212> PRT

<213> Homo sapiens

<400> 280

Thr Pro Ser Cys Ser Ala Ser Ser Ser Pro Cys His Ala Leu Ser Met

1 5 10 15

Pro Trp Pro Pro Met Gly Ser Ser Ser Arg Cys Leu Pro Met Cys Thr 20 25 30

Pro Gly His Arg Cys Leu Trp Arg Ala Pro Trp Arg Ser Gly Ser Ser 35 40 45

Arg Pro Ser Trp His Cys Cys Trp Thr Trp Ser Arg Trp Phe Ser Ser 50 55 60

Cys Pro Leu Ala His Ser Trp Pro Thr His Ser Trp Pro Pro Val Ser 65 70 75 80

Leu Cys Cys Ala Ser Arg Ser Leu Pro Arg Pro Ala Pro Gln Ala Gln 85 90 95

Pro Ala Leu Ala Pro 100

<210> 281

<211> 24

<212> PRT

<213> Homo sapiens

<400> 281

Leu Ser Met Pro Trp Pro Pro Met Gly Ser Ser Ser Arg Cys Leu Pro 1 5 10 15

Met Cys Thr Pro Gly His Arg Cys 20

<210> 282

<211> 27

<212> PRT

<213> Homo sapiens

<400> 282

Ala Pro Trp Arg Ser Gly Ser Ser Arg Pro Ser Trp His Cys Cys Trp 1 5 10 15

PCT/US98/27059

158

Thr Trp Ser Arg Trp Phe Ser Ser Cys Pro Leu 20 25

<210> 283

<211> 22

<212> PRT

<213> Homo sapiens

<400> 283

Thr His Ser Trp Pro Pro Val Ser Leu Cys Cys Ala Ser Arg Ser Leu

1 5 10 15

Pro Arg Pro Ala Pro Gln 20

<210> 284

<211> 60

<212> PRT

<213> Homo sapiens

<400> 284

Ala Tyr Ile Leu Val Ser Thr Val Leu Thr Leu Met Val Pro Trp His

1 5 10 15

Ser Leu Asp Pro Asp Ser Ala Leu Ala Asp Ala Phe Tyr Gln Arg Gly
20 25 30

Tyr Arg Trp Ala Gly Phe Ile Val Ala Ala Gly Ser Ile Cys Ala Met 35 40 45

Asn Thr Val Leu Leu Ser Leu Leu Phe Ser Leu Pro 50 55 60

<210> 285

<211> 31

<212> PRT

<213> Homo sapiens

<400> 285

Pro Trp His Ser Leu Asp Pro Asp Ser Ala Leu Ala Asp Ala Phe Tyr

1 5 10 15

Gln Arg Gly Tyr Arg Trp Ala Gly Phe Ile Val Ala Ala Gly Ser
20 25 30

<210> 286

<211> 27

<212> PRT

<213> Homo sapiens

<400> 286

Arg Ile Val Tyr Ala Met Ala Ala Asp Gly Leu Phe Phe Gln Val Phe 1 5 10 15

```
Ala His Val His Pro Arg Thr Gln Val Pro Val 20 25
```

<210> 287

<211> 16

<212> PRT

<213> Homo sapiens

<400> 287

Asp Leu Glu Ser Leu Val Gln Phe Leu Ser Leu Gly Thr Leu Leu Ala 1 5 10 15

<210> 288

<211> 15

<212> PRT

<213> Homo sapiens

<400> 288

Tyr Thr Phe Val Ala Thr Ser Ile Ile Val Leu Arg Phe Gln Lys 1 5 10 15

<210> 289

<211> 31

<212> PRT

<213> Homo sapiens

<400> 289

Leu Thr Lys Gln Gln Ser Ser Phe Ser Asp His Leu Gln Leu Val Gly

1 5 10 15

Thr Val His Ala Ser Val Pro Glu Pro Gly Glu Leu Lys Pro Ala 20 25 30

<210> 290

<211> 50

<212> PRT

<213> Homo sapiens

<400> 290

Leu Arg Pro Tyr Leu Gly Phe Leu Asp Gly Tyr Ser Pro Gly Ala Val 1 5 10 15

Val Thr Trp Ala Leu Gly Val Met Leu Ala Ser Ala Ile Thr Ile Gly
20 25 30

Cys Val Leu Val Phe Gly Asn Ser Thr Leu His Leu Pro His Trp Gly 35 40 45

Tyr Ile

```
<210> 291
```

<211> 27

<212> PRT

<213> Homo sapiens

<400> 291

Pro Gly Ala Val Val Thr Trp Ala Leu Gly Val Met Leu Ala Ser Ala 1 5 10 15

Ile Thr Ile Gly Cys Val Leu Val Phe Gly Asn 20 25

<210> 292

<211> 53

<212> PRT

<213> Homo sapiens

<400> 292

Gly Ala His Gln Gln Gln Tyr Arg Glu Asp Leu Phe Gln Ile Pro Met

1 5 10 15

Val Pro Leu Ile Pro Ala Leu Ser Ile Val Leu Asn Ile Cys Leu Met 20 25 30

Leu Lys Leu Ser Tyr Leu Thr Trp Val Arg Phe Ser Ile Trp Leu Leu 35 40

Met Gly Leu Ala Val

<210> 293

<211> 26

<212> PRT

<213> Homo sapiens

<400> 293

Met Val Pro Leu Ile Pro Ala Leu Ser Ile Val Leu Asn Ile Cys Leu 1 5 10 15

Met Leu Lys Leu Ser Tyr Leu Thr Trp Val 20 25

<210> 294

<211> 29

<212> PRT

<213> Homo sapiens

<400> 294

Tyr Phe Gly Tyr Gly Ile Arg His Ser Lys Glu Asn Gln Arg Glu Leu

1 5 10 15

Pro Gly Leu Asn Ser Thr His Tyr Val Val Phe Pro Arg 20 25

<210> 295

<211> 23

<212> PRT

<213> Homo sapiens

<400> 295

Phe Pro Pro Ser Pro Ala Pro Pro His Ser Leu Pro Leu Arg Ser Trp

1 5 10 15

Leu Trp Ser Arg Gln Met Gly
20

<210> 296

<211> 148

<212> PRT

<213> Homo sapiens

<400> 296

Gly Thr Ser Phe Arg Gly Met Ile Ser Thr Gln Pro Gly Ser Thr Pro 1 5 10 15

Leu Ala Ser Phe Lys Ile Leu Ala Leu Glu Ser Ala Asp Gly His Gly
20 25 30

Gly Cys Ser Ala Gly Asn Asp Ile Gly Pro Tyr Gly Glu Arg Asp Asp 35

Gln Gln Val Phe Ile Gln Lys Val Val Pro Ser Ala Ser Gln Leu Phe 50 55 60

Val Arg Leu Ser Ser Thr Gly Gln Arg Val Cys Ser Val Arg Ser Val
65 70 75 80

Asp Gly Ser Pro Thr Thr Ala Phe Thr Val Leu Glu Cys Glu Gly Ser 85 90 95

Pro Ala Ala Arg Leu Ser Ala Pro Ala Leu Pro Ala His Trp Pro Gly
100 105 110

Gln Arg Gln Leu Gly His Val Gly Pro Asn His Arg His Gly Arg Pro 115 120 125

Arg Pro Gly Pro Cys Arg Trp Pro Asp Gly Ala Arg Ala Asp Gly Thr 130 135 140

Ala Gly Thr Leu 145

<210> 297

<211> 29

<212> PRT

```
<213> Homo sapiens
<400> 297
 Pro Gly Ser Thr Pro Leu Ala Ser Phe Lys Ile Leu Ala Leu Glu Ser
                                    10
Ala Asp Gly His Gly Gly Cys Ser Ala Gly Asn Asp Ile
<210> 298
<211> 24
<212> PRT
<213> Homo sapiens
<400> 298
Gly Glu Arg Asp Asp Gln Gln Val Phe Ile Gln Lys Val Val Pro Ser
                                    10
Ala Ser Gln Leu Phe Val Arg Leu
            20
<210> 299
<211> 25
<212> PRT
<213> Homo sapiens
<400> 299 ·
Arg Ser Val Asp Gly Ser Pro Thr Thr Ala Phe Thr Val Leu Glu Cys
Glu Gly Ser Pro Ala Ala Arg Leu Ser
           20 . 25
<210> 300
<211> 26
<212> PRT
<213> Homo sapiens
<400> 300
Pro Ala Leu Pro Ala His Trp Pro Gly Gln Arg Gln Leu Gly His Val
Gly Pro Asn His Arg His Gly Arg Pro Arg
            20
<210> 301
<211> 168
<212> PRT
<213> Homo sapiens
<400> 301
Pro Phe Ile Pro Arg Arg Pro Trp Pro Glu Pro Gly Val Pro Thr Gly
```

Ile Arg Glu Ala Pro Glu Ser Pro Arg Thr Arg Ala Ser Gln Gly Ile
20 25 30

Met Ala Ala Leu Phe Lys Lys Glu Val Ser Leu Ser Phe Ile Leu 35 40 45

Gly Gly Val Arg Gly Val Pro Arg Pro Leu Glu Gly His Gly Ala Gly 50 55 60

Val Gly Gly Arg Arg Ser Gly Pro Leu Arg Thr Ser Ser Trp Gln 65 70 75 80

Arg Ser Thr Lys Leu Pro Pro Pro Arg Arg Arg Ala Ser Ala Cys Gly 85 90 95

Gly Leu Gly Leu Pro Arg Trp Pro Asp Lys Glu Val Leu Leu Glu Ala 100 105 110

Glu Trp Arg Leu Val Arg Glu Met Arg Gly Glu Gly Leu Gly Arg Gln 115 120 125

Pro His Glu Gly Ala Glu Arg Ser Arg Arg Gly Gln Leu Thr Val Phe 130 135 140

Gln Leu Phe His Gln Leu Leu Leu Arg Gln Ala Thr Cys Arg Gly Leu 145 150 155 160

Ala Glu Ala Val His Gly Gly Gly 165

<210> 302

<211> 32

<212> PRT

<213> Homo sapiens

<400> 302

Pro Gly Val Pro Thr Gly Ile Arg Glu Ala Pro Glu Ser Pro Arg Thr 1 5 10 15

Arg Ala Ser Gln Gly Ile Met Ala Ala Ala Leu Phe Lys Lys Glu Val 20 25 30

<210> 303

<211> 28

<212> PRT

<213> Homo sapiens

<400> 303

Phe Ile Leu Gly Gly Val Arg Gly Val Pro Arg Pro Leu Glu Gly His

1 5 10 15

164

Gly Ala Gly Val Gly Gly Arg Arg Arg Ser Gly Pro 20 25

<210> 304

<211> 24

<212> PRT

<213> Homo sapiens

<400> 304

Gly Leu Pro Arg Trp Pro Asp Lys Glu Val Leu Leu Glu Ala Glu Trp

1 5 10 15

Arg Leu Val Arg Glu Met Arg Gly 20

<210> 305

<211> 23

<212> PRT

<213> Homo sapiens

<400> 305

Gly Ala Glu Arg Ser Arg Arg Gly Gln Leu Thr Val Phe Gln Leu Phe
1 5 10 15

His Gln Leu Leu Leu Arg Gln 20

<210> 306

<211> 15

<212> PRT

<213> Homo sapiens

<400> 306

His Ala Ser Ala His Ala Ser Ala His Ala Ser Gly Cys Gly Ala
1 5 10 15

<210> 307

<211> 118

<212> PRT

<213> Homo sapiens

<400> 307

Gln Gly Val Gly Val Ala Asp Glu Gly Gly Leu Glu Arg Gln Arg Val

1 5 10 15

Asp Ala Gly Ala Arg Leu Gly His Met Gly Gln Pro Val Ala Phe Ser 20 25 30

Thr Arg Gln Leu His Leu Ala Leu Pro Ala Pro Gly Thr Ala Gly Val

Thr Val Pro His Pro His Ala Arg Glu Gly Val Val Gly Asp Leu Pro 50 55 60

Leu Val Pro Asp Ala Glu Asp Pro Thr Val Gly Val Pro Ala Glu Gly

Leu Leu Val Leu Gly His Val Val Glu Arg Ala Glu Leu Ile Leu Val 90

Arg Gly Leu His Gln Ala Glu Ala Leu Ala Arg Glu Ser Glu Glu Met 105

His Gly Ser Arg His Gly 115

<210> 308

<211> 25

<212> PRT

<213> Homo sapiens

<400> 308

Glu Gly Gly Leu Glu Arg Gln Arg Val Asp Ala Gly Ala Arg Leu Gly

His Met Gly Gln Pro Val Ala Phe Ser 20

<210> 309

<211> 29

<212> PRT

<213> Homo sapiens

<400> 309

Leu Ala Leu Pro Ala Pro Gly Thr Ala Gly Val Thr Val Pro His Pro

His Ala Arg Glu Gly Val Val Gly Asp Leu Pro Leu Val 20

<210> 310

<211> 28

<212> PRT

<213> Homo sapiens

<400> 310

Pro Ala Glu Gly Leu Leu Val Leu Gly His Val Val Glu Arg Ala Glu 5

Leu Ile Leu Val Arg Gly Leu His Gln Ala Glu Ala 20

<210> 311

<211> 125

<212> PRT

<213> Homo sapiens

```
<220>
 <221> SITE
 <222> (32)
 <223> Xaa equals any of the naturally occurring L-amino acids
 His Leu Phe Lys Phe Phe Tyr Thr Ile Ala Phe Met Gln Trp Phe Thr
                                      10
 Glu Phe Met Glu Leu Phe Leu Ser Val Trp Glu Leu Ile Lys Thr Xaa
Asn Leu Cys Phe Val Cys Phe Ser Glu His Lys Pro Gly Gln Leu Val
Pro Ala Gly Pro Thr Ser Gln Leu Leu Cys Arg Ala Leu Gly Arg Val
His Leu Cys Ser Pro Thr Thr Arg Ser Gln Thr Pro Thr Gln Ser Trp
Val Thr Pro Gln Leu Leu Trp Arg Leu Gly Ser Gly Arg Leu Val Ala
Gln Val Leu Gln Val Gly Ser Phe Cys Gly Pro Arg Val Gly Asp Ala
                                105
Val Leu Gly Glu Gln Thr Phe Gln Pro Phe Asp Leu Leu
       115
                           120
<210> 312
<211> 29
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (23)
<223> Xaa equals any of the naturally occurring L-amino acids
<400> 312
Ala Phe Met Gln Trp Phe Thr Glu Phe Met Glu Leu Phe Leu Ser Val
Trp Glu Leu Ile Lys Thr Xaa Asn Leu Cys Phe Val Cys
            20
<210> 313
<211> 26
<212> PRT
<213> Homo sapiens
Arg Ser Gln Thr Pro Thr Gln Ser Trp Val Thr Pro Gln Leu Leu Trp
```

```
WO 99/31117 PCT/US98/27059
```

167 1 5 10 15

Arg Leu Gly Ser Gly Arg Leu Val Ala Gln
20 25

<210> 314

<211> 39

<212> PRT

<213> Homo sapiens

<400> 314

Gly Ala Trp Gly Val Glu Val Val Ala Val Gly Ser Lys Ala Gly Cys

1 5 10 15

Leu Val Tyr Gln Leu Cys Asp Leu Lys Gln Ile Thr Phe Phe Phe Arg
20 25 30

Ala Ser Val Cys Leu Ser Val 35

<210> 315

<211> 194

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (61)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (95)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (116)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (129)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (131)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (132)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (163)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (187)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 315

Pro Ala Ser Leu Gly Ser Ser Trp Gly Gln Lys Leu Arg Gly Gly Thr

1 5 10 15

Arg Lys Ser Phe Gln Glu Leu Ser Pro Ser Ser Ala Pro Pro Ala Cys 20 25 30

Leu Pro Gln Pro Pro Ala Ser Thr Trp Leu Ser Ser Trp Pro Arg Pro 35 40 45

Pro Cys Trp Pro Pro Met Cys Ser Trp Ala Leu Gly Xaa Cys Phe Cys 50 55 60

Pro Ala Thr Gly Gln Trp Leu Pro Thr Ser Cys Cys Leu Trp Trp Cys 65 70 75 80

Pro Asp Ala Gly Gly Arg Gln Lys His Phe Arg Ser Arg Trp Xaa Thr 85 90 95

Ser Trp Glu Thr Trp Gln Pro Tyr Leu Thr Gly Leu Ile Ser Ser Val 100 105 110

Leu Arg Ala Xaa Arg Pro Asp Ser Tyr Leu Gln Arg Phe Arg Ser Leu 115 120 125

Xaa Gln Xaa Xaa Leu Cys Cys Ala Phe Val Ile Ala Leu Gly Gly 130 135 140

Cys Phe Leu Leu Thr Ala Leu Tyr Leu Glu Arg Asp Glu Thr Arg Ala 145 150 155 160

Trp Gln Xaa Val Thr Gly Thr Pro Asp Ser Asn Asp Val Asp Ser Asn 165 170 175

Asp Leu Glu Arg Gln Gly Leu Leu Ser Gly Xaa Gly Ala Ser Thr Glu 180 185 190

Glu Pro

<210> 316

<211> 26

<212> PRT

<213> Homo sapiens

<400> 316

169 Leu Arg Gly Gly Thr Arg Lys Ser Phe Gln Glu Leu Ser Pro Ser Ser 5 Ala Pro Pro Ala Cys Leu Pro Gln Pro Pro 20 <210> 317 <211> 28 <212> PRT <213> Homo sapiens <400> 317 Ala Thr Gly Gln Trp Leu Pro Thr Ser Cys Cys Leu Trp Trp Cys Pro 10 Asp Ala Gly Gly Arg Gln Lys His Phe Arg Ser Arg 20 <210> 318 <211> 22 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (21) <223> Xaa equals any of the naturally occurring L-amino acids <400> 318 Gly Gly Cys Phe Leu Leu Thr Ala Leu Tyr Leu Glu Arg Asp Glu Thr 10 Arg Ala Trp Gln Xaa Val 20 <210> 319 <211> 124 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (38) <223> Xaa equals any of the naturally occurring L-amino acids <220> <221> SITE <222> (72) <223> Xaa equals any of the naturally occurring L-amino acids

<223> Xaa equals any of the naturally occurring L-amino acids

<220> <221> SITE <222> (76)

```
<220>
<221> SITE
<222> (93)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (105)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (106)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (107)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (109)
<223> Xaa equals any of the naturally occurring L-amino acids
<400> 319
Ala Pro His Leu Arg Leu Gln Pro Ala Cys His Ser Pro Leu Pro Leu
                  5
                                     10
Pro Gly Ser Arg Pro Gly Pro Asp His Pro Ala Gly Leu Leu Cys Val
Pro Gly Pro Trp Gly Xaa Ala Ser Val Leu Gln Leu Gly Ser Gly Cys
                             40
Arg His Pro Ala Val Cys Gly Gly Ala Gln Met Pro Gly Asp Gly Arg
Ser Thr Ser Asp His Gly Gly Xaa His Pro Gly Xaa Pro Gly Ser Pro
Ile Ser Gln Asp Leu Ser Leu Val Ser Cys Gly Pro Xaa Ala Leu Thr
                 85
                                     90
Pro Ile Cys Ser Ala Ser Ala Ala Xaa Xaa Xaa Xaa Cys Ala Ala
            100
                                105
Pro Leu Ser Ser Pro Trp Gly Ala Ala Ala Ser Cys
        115
```

SUBSTITUTE SHEET (RULE 26)

```
<210> 320
<211> 25
<212> PRT
```

<213> Homo sapiens

<400> 320

Pro Ala Cys His Ser Pro Leu Pro Leu Pro Gly Ser Arg Pro Gly Pro 1 5 10 15

Asp His Pro Ala Gly Leu Leu Cys Val 20 25

<210> 321 <211> 26

<212> PRT

<213> Homo sapiens

<400> 321

Ser Gly Cys Arg His Pro Ala Val Cys Gly Gly Ala Gln Met Pro Gly
1 5 10 15

Asp Gly Arg Ser Thr Ser Asp His Gly Gly 20 25

<210> 322

<211> 95

<212> PRT

<213> Homo sapiens

<400> 322

Gly Leu Lys Val Met Glu Ile Cys Ser Leu Thr Phe Leu Glu Ala Thr 1 5 10 15

Asn Leu Gln Ser Arg Cys Gln Gln Ala Met Leu Pro Leu Lys Ala Leu 20 25 30

Arg Lys Asn Pro Phe Leu Leu Leu Pro Ser Phe Asp Gly Cys Cys Gln 35 40 45

Ser Leu Ala Phe Pro Gly Leu Trp Leu Gln His Ser Asn Leu Cys Leu 50 60

Asn His His Met Thr Phe Leu Val Tyr Leu Leu Cys Val Ser Val Phe 65 70 75 80

Lys Tyr Phe Phe Pro Phe Ser Cys Thr Tyr Thr Ser His Trp Ile 85 90 95

<210> 323

<211> 22

<212> PRT

<213> Homo sapiens

<400> 323

172

Ile Cys Ser Leu Thr Phe Leu Glu Ala Thr Asn Leu Gln Ser Arg Cys

1 5 10 15

Gln Gln Ala Met Leu Pro 20

<210> 324

<211> 26

<212> PRT

<213> Homo sapiens

<400> 324

Gly Leu Trp Leu Gln His Ser Asn Leu Cys Leu Asn His His Met Thr 1 5 10 15

Phe Leu Val Tyr Leu Leu Cys Val Ser Val 20 25

<210> 325

<211> 37

<212> PRT

<213> Homo sapiens

<400> 325

Pro Phe Pro Leu Leu Pro Pro Lys Arg Arg Gly Leu Leu Tyr His Leu 1 5 10 15

Ile Gln Lys Ser Thr Leu Gly Leu Val Val Trp Phe Arg Glu His Leu 20 25 30

Asp Ser Arg Ser Gln 35

<210> 326

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (46)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (48)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (65)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 326

Arg Gly Xaa Pro Ser Trp Pro Met His Thr Leu Val Tyr Ala Gln His 1 5 10 15

Ser Thr Thr His Thr Pro Leu Ile Gln Pro Gln Trp Thr Gln Val Ile
20 25 30

Asp Gln Pro Pro Gly Ile Thr His Gln Phe Cys Val Arg Xaa Cys Xaa 35 40 45

Cys Pro Thr Leu Glu Ser Cys Val Gln Glu Cys Val Thr Arg Ser Arg 50 55 60

Xaa Lys Pro Thr Thr Gly Val Pro Gly Pro Gln Arg Leu Ala 65 70 75

<210> 327

<211> 24

<212> PRT

<213> Homo sapiens

<400> 327

Thr Pro Leu Ile Gln Pro Gln Trp Thr Gln Val Ile Asp Gln Pro Pro 1 5 10 15

Gly Ile Thr His Gln Phe Cys Val

<210> 328

<211> 104

<212> PRT

<213> Homo sapiens

<400> 328

Ala Leu Gly Pro Ser Gln Thr Cys Asp Leu Asp Val Trp Leu Val Ala 1 5 10 15

Lys Pro Ser Phe Phe Arg Gly Pro Gln Gly Ile His Tyr Phe Ser Leu 20 25 30

Trp Arg Arg Lys Pro Leu Ser His Trp Val Ser Ile Trp Gln Leu Gln 35 40 45

Gly Gln Glu Thr Met Pro Ala Met Leu Arg Ser Arg Pro Ala Gly Gln 50 60

Ala Thr Val Ala Thr Gly Pro Pro Arg Gly Ser Pro Ser Pro Gln Asp
65 70 75 80

Leu Pro Ser Tyr His Arg Lys Gln Val Glu Ser Ser His Arg His Ser 85 90 95

SUBSTITUTE SHEET (RULE 26)

```
Trp Glu Pro Ala Ser Gln Ser Gln
           100
<210> 329
<211> 28
<212> PRT
<213> Homo sapiens
<400> 329
Cys Asp Leu Asp Val Trp Leu Val Ala Lys Pro Ser Phe Phe Arg Gly
                 5
Pro Gln Gly Ile His Tyr Phe Ser Leu Trp Arg Arg
             20
                                  25
<210> 330
<211> 28
<212> PRT
<213> Homo sapiens
<400> 330
Ala Gly Gln Ala Thr Val Ala Thr Gly Pro Pro Arg Gly Ser Pro Ser
Pro Gln Asp Leu Pro Ser Tyr His Arg Lys Gln Val
             20
<210> 331
<211> 79
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids
Xaa Gly Asp Thr Xaa Thr Gln Asn Ser Arg His Asp Thr Pro Xaa Leu
Ile Asp Tyr Tyr Arg Glu Ser Cys Thr Leu Gln Tyr Arg Pro Glu Phe
             20
```

Pro Gly Arg Pro Thr Arg Pro Arg Gly Ser Cys Pro Gln Tyr Pro Gly 35 40 45

Pro Ala Ile Pro Arg Thr Ser Trp Ala Leu Gly Glu Gly Asp Ala Ala 50 55 60

Pro Arg Gly Ala His His Pro Arg Arg Ala Asp Val Pro Leu Gly 65 70 75

<210> 332

WO 99/31117

<211> 30

<212> PRT

<213> Homo sapiens

<400> 332

Tyr Arg Glu Ser Cys Thr Leu Gln Tyr Arg Pro Glu Phe Pro Gly Arg

1 5 10 15

Pro Thr Arg Pro Arg Gly Ser Cys Pro Gln Tyr Pro Gly Pro
20 25 30

<210> 333

<211> 155

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (72)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 333

Gly Lys Leu Tyr Ala Ala Val Pro Ser Gly Ile Pro Gly Ser Thr His

1 5 10 15

Ala Ser Ala Arg Leu Met Pro Pro Val Ser Arg Ser Ser Tyr Ser Glu 20 25 30

Asp Ile Val Gly Ser Arg Arg Arg Arg Ser Ser Ser Gly Ser Pro 35 40 45

Pro Ser Pro Gln Ser Arg Cys Ser Ser Trp Asp Gly Cys Ser Arg Ser 50 55 60

His Ser Arg Gly Arg Glu Gly Xaa Arg Pro Pro Trp Ser Glu Leu Asp 65 70 75 80

Val Gly Ala Leu Tyr Pro Phe Ser Arg Ser Gly Ser Arg Gly Arg Leu 85 90 95

Pro Arg Phe Arg Asn Tyr Ala Phe Ala Ser Ser Trp Ser Thr Ser Tyr 100 105 110

Ser Gly Tyr Arg Tyr His Arg Ala Leu Leu Cys Arg Arg Thr Ala Val

SUBSTITUTE SHEET (RULE 26)

115

120

125

Ser Gly Arg Leu Arg Glu Gly Arg Glu Pro Ser Ala Glu Glu Ala Glu 130 135 140

Gly Glu Arg Glu Asp Trp Gly Ile Gly Ser Ala 145 150 155

<210> 334

<211> 23

<212> PRT

<213> Homo sapiens

<400> 334

Ser Gly Ile Pro Gly Ser Thr His Ala Ser Ala Arg Leu Met Pro Pro 1 5 10 15

Val Ser Arg Ser Ser Tyr Ser 20

<210> 335

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (13)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 335

Gly Cys Ser Arg Ser His Ser Arg Gly Arg Glu Gly Xaa Arg Pro Pro 1 5 10 15

Trp Ser Glu Leu Asp Val Gly Ala Leu Tyr Pro Phe Ser

<210> 336

<211> 25

. <212> PRT

<213> Homo sapiens

<400> 336

Thr Ala Val Ser Gly Arg Leu Arg Glu Gly Arg Glu Pro Ser Ala Glu

1 5 10 15

Glu Ala Glu Gly Glu Arg Glu Asp Trp
20 25

<210> 337

<211> 134

<212> PRT

<213> Homo sapiens

```
<220>
 <221> SITE
 <222> (17)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (77)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <400> 337
 Arg Ile Arg Lys Ala Ala Val Gln Ile Pro Thr Arg Lys Asn Ile Gly
Xaa Arg Arg Pro Val Val Gln Glu Thr Arg Lys Lys Glu Arg Ile Ser
             20
Arg Leu Lys Glu Ser Ile Gly Asn Ile Leu Ile Val Thr Val Thr Gln
                              40
Ser Leu Thr Gln Ile Leu Thr Leu Met Met Ile Lys Arg Glu Leu Lys
                                              60
Pro Arg Arg Lys Arg Arg Asn Thr Lys Gln Xaa Lys Arg Arg
Ile Arg Lys Pro Lys Lys Asn Pro Val Thr Gln Ala Val Lys Thr Gln
                 85
Lys Arg Thr Cys Gln Lys Leu Pro Gly Met Glu Gln Pro Asn Val Ala
                                105
Asp Thr Met Asp Leu Ile Gly Pro Glu Ala Pro Ile Asn Thr Tyr Leu
                            120
Phe Lys Met Lys Asn Leu
    130
<210> 338
<211> 28
<212> PRT
<213> Homo sapiens
<400> 338
Thr Arg Lys Lys Glu Arg Ile Ser Arg Leu Lys Glu Ser Ile Gly Asn
                                    10
Ile Leu Ile Val Thr Val Thr Gln Ser Leu Thr Gln
             20
<210> 339
<211> 28
<212> PRT
```

SUBSTITUTE SHEET (RULE 26)

<213> Homo sapiens

```
<400> 339
Val Lys Thr Gln Lys Arg Thr Cys Gln Lys Leu Pro Gly Met Glu Gln
Pro Asn Val Ala Asp Thr Met Asp Leu Ile Gly Pro
<210> 340
<211> 80
<212> PRT
<213> Homo sapiens
<400> 340
Leu Pro Phe Thr Leu Lys Pro Lys Met Val Lys Ile Pro Phe Ser Ser
                 5
Arg Leu Ile Asn Asn Asn Leu Gln Tyr Ile Asp Cys Ile Leu Ser Leu
Lys Arg Cys Glu Glu Ile Leu Leu Met Trp His Gly Leu Leu Cys
                             40
Leu Ala Ser Val Phe Leu Glu Leu Arg Gly Asp Arg Pro Pro Leu Leu
Ala Ser Leu Leu Glu Pro His Lys Met Pro Leu His Ser Ser Ser Leu
                   70
<210> 341
<211> 24
<212> PRT
<213> Homo sapiens
Leu Lys Pro Lys Met Val Lys Ile Pro Phe Ser Ser Arg Leu Ile Asn
            5
Asn Asn Leu Gln Tyr Ile Asp Cys
             20
<210> 342
<211> 23
<212> PRT
<213> Homo sapiens
<400> 342
Ser Leu Lys Arg Cys Glu Glu Ile Leu Leu Met Trp His Gly Leu Leu
                 5
```

SUBSTITUTE SHEET (RULE 26)

Leu Cys Leu Ala Ser Val Phe

```
<210> 343
 <211> 21
 <212> PRT
 <213> Homo sapiens
 <400> 343
 Leu Arg Gly Asp Arg Pro Pro Leu Leu Ala Ser Leu Leu Glu Pro His
 Lys Met Pro Leu His
              20
 <210> 344
 <211> 79
 <212> PRT
 <213> Homo sapiens
 <400> 344
 Leu Gln Met His Thr Gly Ser Gly Phe Lys Gly Lys Ser Cys Glu Val
Ala Phe Tyr Val Ala Gln Ala Glu Lys Pro Gly Glu Gly Ala Tyr Leu
His Gly Ala Gln Glu Thr Gln Lys Gln Gly Ile Glu Ala Asp His Ala
         35
Thr Leu Arg Gly Ser Pro His Ser Val Ser Lys Thr Lys Tyr Asn Leu
Tyr Ile Ala Asn Tyr Tyr Leu Leu Ala Trp Arg Lys Met Glu Ser
<210> 345
<211> 20
<212> PRT
<213> Homo sapiens
<400> 345
Cys Glu Val Ala Phe Tyr Val Ala Gln Ala Glu Lys Pro Gly Glu Gly
Ala Tyr Leu His
```

<210> 346 <211> 23

-212 DD

<212> PRT

<213> Homo sapiens

<400> 346

180

Ala Thr Leu Arg Gly Ser Pro His Ser Val Ser Lys Thr Lys Tyr Asn 1 5 10 15

Leu Tyr Ile Ala Asn Tyr Tyr
20

<210> 347

<211> 65

<212> PRT

<213> Homo sapiens

<400> 347

Leu Ser Ala Ser Leu Leu Asp Arg Tyr Pro Ala Ser Glu Ser Asn Asn 1 5 10 15

Tyr Ile Phe Asn Phe Val Leu Tyr Met Leu His Phe Leu Ala Gly Thr
20 25 30

Leu Phe Ser Leu Phe Pro Asp Phe Glu Leu Ser Pro Arg Ser Ala Thr
35 40 45

Leu Phe Pro Asp Leu Arg Thr Val Gln Leu Leu Ser Ser Arg Pro His 50 55 60

Leu

65 ;

<210> 348

<211> 23

<212> PRT

<213> Homo sapiens

<400> 348

Leu Leu Asp Arg Tyr Pro Ala Ser Glu Ser Asn Asn Tyr Ile Phe Asn 1 5 10 15

Phe Val Leu Tyr Met Leu His
20

<210> 349

<211> 20

<212> PRT

<213> Homo sapiens

<400> 349

Phe Pro Asp Phe Glu Leu Ser Pro Arg Ser Ala Thr Leu Phe Pro Asp 1 5 10 15

Leu Arg Thr Val

20

<210> 350

<211> 85

```
<212> PRT
```

<213> Homo sapiens

<400> 350

Asn Gly Gly Phe Tyr Asp Val Ser Phe Lys Gln Ala Gly Leu Ile Glu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Phe Leu Cys Ile Ile Tyr Phe Tyr Pro Met Ala His Val Ile Cys Gly
20 25 30

Ser Arg Phe Thr Ile Val Arg Thr Ile Pro Val His Tyr Val Gly Glu 35 40 45

Tyr Phe Ile Lys Ser Ser Ile Trp Ile Leu Tyr Arg Ile Asn Glu Arg
50 55 60

Thr Ala Thr Lys Lys Ala Ala Ser Asp Phe Gln Lys Asn Phe Arg Cys 65 70 75 80

Phe Leu Asp Ala Phe

<210> 351

<211> 19

<212> PRT

<213> Homo sapiens

<400> 351

Lys Gln Ala Gly Leu Ile Glu Phe Leu Cys Ile Ile Tyr Phe Tyr Pro 1 5 10 15

Met Ala His

<210> 352

<211> 23

<212> PRT

<213> Homo sapiens

<400> 352

Tyr Phe Ile Lys Ser Ser Ile Trp Ile Leu Tyr Arg Ile Asn Glu Arg

1 5 10 15

Thr Ala Thr Lys Lys Ala Ala 20

<210> 353

<211> 22

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

```
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
 <222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids
Ser Pro Arg Xaa Gly Arg Xaa Phe Xaa Thr Ser Arg Lys Gln Ile Ser
Gly Phe Leu Glu Phe Asp
             20
<210> 354
<211> 56
<212> PRT
<213> Homo sapiens
<400> 354
Met Lys His Ala Ala Phe Gly Leu Ile Pro Leu Val Lys Glu Ile Tyr
                                      10
Arg Tyr Leu Lys Ile Lys Ser Lys Leu Leu Ile Gly Ser Gly Lys Cys
                                 25
Gln Leu Gln Pro Glu Trp Leu Gln Thr Ser Leu Ile Asn Ser Ser Leu
Leu Met Asp Trp Leu Thr Pro Tyr
<210> 355
<211> 29
<212> PRT
<213> Homo sapiens
<400> 355
Ile Tyr Arg Tyr Leu Lys Ile Lys Ser Lys Leu Leu Ile Gly Ser Gly
                  5
Lys Cys Gln Leu Gln Pro Glu Trp Leu Gln Thr Ser Leu
            20
<210> 356
<211> 68
<212> PRT
<213> Homo sapiens
```

<400> 356
Gln Leu Gly Leu Pro Trp Asp Gln Ser Lys Gly Pro Arg Lys Asn Gly

Leu Ser Met Cys Gly Ser Val Tyr Ser Thr Ile Trp Ser Leu Ile Ala 20 25 30

Ser Arg Arg Glu Glu Thr Ile Arg Val Ile Val Leu Tyr Ile Gln Ser 35 40 45

Pro Asn Ile Asn Thr Arg His Ile Ser Lys Arg Gly Leu Asn Lys Ala 50 55 60

Leu Thr Asn Pro 65

<210> 357

<211> 21

<212> PRT

<213> Homo sapiens

<400> 357

Ser Lys Gly Pro Arg Lys Asn Gly Leu Ser Met Cys Gly Ser Val Tyr

1 5 10 15

Ser Thr Ile Trp Ser 20

<210> 358

<211> 17

<212> PRT

<213> Homo sapiens

<400> 358

Gln Ser Pro Asn Ile Asn Thr Arg His Ile Ser Lys Arg Gly Leu Asn
1 5 10 15

Lys

<210> 359

<211> 19

<212> PRT

<213> Homo sapiens

<400> 359

His Pro Gln Thr Ser Ala Gly Gly Phe Pro Leu His Gln Gly Leu Pro
1 5 10 15

Thr Val Ser

<210> 360

```
184
 <211> 117
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (110)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <400> 360
Pro Ser Trp Phe Pro Glu Leu Ser Pro Trp Pro Leu Lys Thr Leu Lys
Lys Arg Arg Gln Met Arg Leu Arg Arg Gly Arg Leu Cys Arg Leu
Ser Pro Ala Thr Thr Thr Ala Asp Thr Cys Arg Cys Pro Ala Arg
Ser Tyr Arg Gly Ser Gly Arg Arg Pro Ala Cys Ala Gln Asp Ser Pro
                          55 .
Ala Pro Pro Ser Arg Pro Thr Arg Arg Ala Trp Glu Lys Cys Ala Leu
Arg Pro Lys Arg Ala Ala Gln Trp Ser Thr Gly Val Pro Pro Ser Pro
Arg Ser Ser Thr Thr Gly Cys Cys Phe Gly Thr Ala Ala Xaa Cys Ala
        100
Glu Gly Ala Arg Arg
        115
<210> 361
<211> 22
<212> PRT
<213> Homo sapiens
<400> 361
Thr Thr Thr Ala Asp Thr Cys Arg Cys Pro Ala Arg Ser Tyr Arg Gly
Ser Gly Arg Arg Pro Ala
<210> 362
<211> 24
<212> PRT
<213> Homo sapiens
<400> 362
```

Pro Ser Arg Pro Thr Arg Arg Ala Trp Glu Lys Cys Ala Leu Arg Pro

5

PCT/US98/27059

Lys Arg Ala Ala Gln Trp Ser Thr 20

<210> 363

<211> 20

<212> PRT

<213> Homo sapiens

<400> 363

Ala Arg Gly Val Leu Asn Leu Arg Asn Arg Phe Glu Cys Phe Ser Ile

1 5 10 15

Ile Glu Thr Val

<210> 364

<211> 69

<212> PRT

<213> Homo sapiens

<400> 364

Ile Gly Gln Leu Val Met Lys Ser Ile Cys His Phe Gln Arg Leu Leu
1 5 10 15

Ser Val Ala Ile Asp Phe Ala Ser Gln Phe Leu Lys Asn Tyr Ile Phe
20 25 30

Ser Ser Thr His Ser Ser Lys Ala Gly Phe Ser Val Val Cys Ser Leu
35 40 45

Pro Lys Trp Leu Tyr Thr Asp Gly Met Glu Met Val Leu Lys Ile Thr 50 55 60

His Lys Leu Ser Phe

<210> 365

<211> 24

<212> PRT

<213> Homo sapiens

<400> 365

Gln Arg Leu Leu Ser Val Ala Ile Asp Phe Ala Ser Gln Phe Leu Lys

1 5 10 15

Asn Tyr Ile Phe Ser Ser Thr His

<210> 366

<211> 12

<212> PRT

<213> Homo sapiens

<400> 366 Leu Met Lys Thr Ala Ser Arg Met Leu Leu Glu <210> 367 <211> 25 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (3) <223> Xaa equals any of the naturally occurring L-amino acids <220> <221> SITE <222> (6) <223> Xaa equals any of the naturally occurring L-amino acids <400> 367 Ala Thr Xaa Trp Asp Xaa Pro Gly Cys Arg Asn Ser Ala Arg Gly Glu Arg Leu His Val Gly Asp Ala Pro Trp 20 <210> 368 <211> 109 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (102) <223> Xaa equals any of the naturally occurring L-amino acids <220> <221> SITE <222> (105) <223> Xaa equals any of the naturally occurring L-amino acids <400> 368 Ala Arg Asp Glu Arg Arg Glu Val Leu Lys Thr Leu Met Arg Leu Ser Thr Gln Arg Pro Gln Ala Phe Leu Pro Ser Gln Ser Trp Phe Val Arg 20 25 Leu Gln Lys Ala Gly Glu Gly Ala Leu Lys Gln Glu Asn Ser Leu Thr Ile Gln Asn Cys Leu Leu Cys Leu Pro Arg Val His Arg Gln Arg Pro 50 55 Thr Pro Pro Gln Pro Gln Arg Gly Asn Thr Glu Ala Ser Val Leu Gln

SUBSTITUTE SHEET (RULE 26)

65 70 75 80

Thr Ser Thr Glu His Leu Pro Arg Ala Ala Val Leu Leu Val Pro Asn 85 90 95

Ser Cys Ser Pro Gly Xaa Pro Thr Xaa Leu Leu Ser Ser 100 105

<210> 369

<211> 22

<212> PRT

<213> Homo sapiens

<400> 369

Glu Arg Arg Glu Val Leu Lys Thr Leu Met Arg Leu Ser Thr Gln Arg

1 5 10 15

Pro Gln Ala Phe Leu Pro 20

<210> 370

<211> 25

<212> PRT

<213> Homo sapiens

<400> 370

Gly Ala Leu Lys Gln Glu Asn Ser Leu Thr Ile Gln Asn Cys Leu Leu 1 5 10 15

Cys Leu Pro Arg Val His Arg Gln Arg 20 25

<210> 371

<211> 21

<212> PRT

<213> Homo sapiens

<400> 371

Ser Val Leu Gln Thr Ser Thr Glu His Leu Pro Arg Ala Ala Val Leu

1 5 10 15

Leu Val Pro Asn Ser 20

<210> 372

<211> 9

<212> PRT

<213> Homo sapiens

<400> 372

Ala Leu Val Ile Ser Asn Pro Leu Leu 1 5

```
<210> 373
 <211> 63
 <212> PRT
 <213> Homo sapiens
 <400> 373
 Pro Tyr Ile Asn Thr Gln Met Cys Val Ser Ser Arg Asn Lys Phe Cys
 Ile Ser Gly His Gln Lys Tyr Asp Ser His Gly Arg Glu Thr Arg Phe
                                  25
 Glu Met His Lys Ala Arg Ala Ser Ser Trp Lys Asn Ile Leu Lys Ile
 Arg Ser Leu Lys Ile Ile Ser Arg Gly Phe Glu Ile Thr Asn Ala
                          55
 <210> 374
 <211> 27
 <212> PRT
 <213> Homo sapiens
<400> 374
Lys Phe Cys Ile Ser Gly His Gln Lys Tyr Asp Ser His Gly Arg Glu
Thr Arg Phe Glu Met His Lys Ala Arg Ala Ser
             20
<210> 375
<211> 84
<212> PRT
<213> Homo sapiens
<400> 375
His Thr Leu Leu Glu Ile Ala Asn Pro Leu Gln Ala Ala Val Leu Gly
Ala Ser Ser Ile His Pro Ser Ile His Thr Ser Thr His Leu Met Phe
                                 25
Met Gly Leu Lys Trp Thr Glu Leu His His Ser Pro Asp Ser Val Gln
Gly Ala Gly Ala Ala Glu Ala Ala Gln Thr Arg His Ser Leu Arg Pro
```

Phe Ile Ile Cys

Gly Arg Gly Arg Glu Arg His Asp Cys Thr Leu Lys Asn Leu Thr Leu

```
<210> 376
   <211> 22
   <212> PRT
   <213> Homo sapiens
   <400> 376
  Asn Pro Leu Gln Ala Ala Val Leu Gly Ala Ser Ser Ile His Pro Ser
                                       10
  Ile His Thr Ser Thr His
  <210> 377
  <211> 17
  <212> PRT
  <213> Homo sapiens
  <400> 377
  Ser Leu Arg Pro Gly Arg Gly Arg Glu Arg His Asp Cys Thr Leu Lys
                                        10
  Asn
 <210> 378
  <211> 52
 <212> PRT
 <213> Homo sapiens
 <400> 378
 Ala Glu Asn Val His Cys Thr Pro Ala Trp Glu Thr Gly Arg Asp Ser
 Glu Asp Gly Lys Gly Arg Glu Gly Met Gly Arg Asp Arg Lys Gly Trp
                                                      30
 Asp Gly Thr Gly Leu Asp Gly Thr Gly Trp Glu Gly Lys Arg Glu Arg
                              40
Asn Val Pro Ala
      50
 <210> 379
<211> 26
<212> PRT
<213> Homo sapiens
<400> 379
Gly Arg Asp Ser Glu Asp Gly Lys Gly Arg Glu Gly Met Gly Arg Asp
Arg Lys Gly Trp Asp Gly Thr Gly Leu Asp
             20
```

```
<210> 380
<211> 14
<212> PRT
 <213> Homo sapiens
<400> 380
Thr Ser Leu Gly Asp Leu Trp Asp Tyr Asn Asn Ser Ser His
                 5
<210> 381
<211> 66
<212> PRT
<213> Homo sapiens
<400> 381
Asp Arg Arg Ile Ile Arg Thr Arg Glu Ala Ala Val Ala Val Ser Arg
Glu Arg Pro Leu His Ser Ser Leu Gly Asn Arg Glu Arg Leu Arg Arg
             20
                                25
Trp Glu Gly Thr Gly Arg Asp Gly Lys Gly Gln Glu Gly Met Gly Arg
Asp Gly Thr Gly Trp Asp Gly Met Gly Arg Glu Glu Arg Lys Lys Cys
Pro Ser
 65
<210> 382
<211> 25
<212> PRT
<213> Homo sapiens
<400> 382
Arg Pro Leu His Ser Ser Leu Gly Asn Arg Glu Arg Leu Arg Arg Trp
            5
Glu Gly Thr Gly Arg Asp Gly Lys Gly
<210> 383
<211> 9
<212> PRT
<213> Homo sapiens
<400> 383
Asn Gln Ser Trp Gly Pro Met Gly Leu
           5
```

```
WO 99/31117
                                      191
 <210> 384
 <211> 59
 <212> PRT
 <213> Homo sapiens
 <400> 384
 Gly Gly Gly Cys Ser Glu Pro Arg Thr Ser Ile Ala Leu Gln Pro
                   5
 Gly Lys Gln Gly Glu Thr Pro Lys Met Gly Arg Asp Gly Lys Gly Trp
 Glu Gly Thr Gly Arg Asp Gly Thr Gly Arg Asp Trp Met Gly Arg Asp
                              40
 Gly Lys Gly Arg Glu Lys Glu Met Ser Gln Gln
 <210> 385
<211> 24
<212> PRT
<213> Homo sapiens
<400> 385
Lys Gln Gly Glu Thr Pro Lys Met Gly Arg Asp Gly Lys Gly Trp Glu
Gly Thr Gly Arg Asp Gly Thr Gly
             20
<210> 386
<211> 32
<212> PRT
<213> Homo sapiens
<400> 386
Pro Val Leu Gly Thr Tyr Gly Thr Ile Thr Thr Pro Val Thr Glu Leu
                  5
Thr Lys Gly Gln Glu Lys Glu Gly Gly Val Glu Thr Val Leu Tyr Glu
             20
<210> 387
```

<211> 11 <212> PRT <213> Homo sapiens <400> 387 Lys Ile Val Phe Ile Asp Gln Lys Trp Ser Lys 1 5 10

```
<210> 388
 <211> 70
 <212> PRT
 <213> Homo sapiens
 <400> 388
 Cys Ser Leu Phe Trp Gly Ile Leu Phe Leu Ser Arg Leu Arg Ile His
 Leu Phe Leu Ser Leu Lys Pro Cys Met Cys Leu Arg Pro Ile Asp Ile
 Leu Ser His Phe Leu Asp Ile Phe Val Thr Ser Val Leu Ser Glu Leu
                             40
 Glu Lys Ser Ser Leu Lys Thr Thr Glu Thr Phe Ser Phe Ala Val Phe
                 55
Leu Leu Met Met Asn
<210> 389
<211> 26
<212> PRT
<213> Homo sapiens
<400> 389
Leu Ser Arg Leu Arg Ile His Leu Phe Leu Ser Leu Lys Pro Cys Met
Cys Leu Arg Pro Ile Asp Ile Leu Ser His
            20
<210> 390
<211> 22
<212> PRT
<213> Homo sapiens
<400> 390
Val Leu Ser Glu Leu Glu Lys Ser Ser Leu Lys Thr Thr Glu Thr Phe
                      10
Ser Phe Ala Val Phe Leu
           20
<210> 391
<211> 8
<212> PRT
<213> Homo sapiens
<400> 391
Thr Leu Phe Arg Tyr Ile Leu His
```

SUBSTITUTE SHEET (RULE 26)

1 5

```
<210> 392
 <211> 14
 <212> PRT
 <213> Homo sapiens
 <400> 392
 Gly Thr Ser Phe Ser Val Leu Ser Leu Ile His Asp Thr Gly
 1 5
 <210> 393
 <211> 63
 <212> PRT
 <213> Homo sapiens
<400> 393
Val Leu Ile Ser Ala Ser Thr Ile Gly Ser Arg Thr Ser Gly Ala Gln
Gly Met Glu Lys Met Thr Ile Pro Thr Leu Ala Val Gly Glu Pro Lys
                                25
Thr Pro Glu Lys Ser Lys Cys Ser Leu Lys Gln Cys Phe Ser Ser Cys
                             40
Asn Val His Ile Asp His Leu Gly Leu Leu Leu Lys Cys Lys Phe
<210> 394
<211> 23
<212> PRT
<213> Homo sapiens
<400> 394
Ala Ser Thr Ile Gly Ser Arg Thr Ser Gly Ala Gln Gly Met Glu Lys
                                   10
Met Thr Ile Pro Thr Leu Ala
            20
<210> 395
<211> 27
<212> PRT
<213> Homo sapiens
<400> 395
Gly Glu Pro Lys Thr Pro Glu Lys Ser Lys Cys Ser Leu Lys Gln Cys
Phe Ser Ser Cys Asn Val His Ile Asp His Leu
```

<210> 396 <211> 101

<212> PRT

<213> Homo sapiens

<400> 396

Arg Ile Arg Ser Gln Asp Leu Ala Ile Met Thr Thr Cys Phe Lys Lys

Tyr Glu Phe Ser Phe Phe Val Leu Gly Phe Leu Arg Arg Trp Gly Ala 25

Thr Leu Cys Leu Gly Phe Thr Ser Phe Ala Ile Lys Phe His Pro Ser

Ser Leu Cys Ser Glu Lys Glu Gly Lys Asp Phe Ser Gly Phe Ala Leu

Ser Ile His Gly Pro Glu Arg Lys Lys Glu Glu Gly Trp Ala Arg Trp

Leu Thr Pro Val Val Pro Val Leu Trp Glu Ala Glu Val Gly Ser

Pro Glu Val Ser Ser 100

<210> 397

<211> 22

<212> PRT

<213> Homo sapiens

<400> 397

Thr Thr Cys Phe Lys Lys Tyr Glu Phe Ser Phe Phe Val Leu Gly Phe

Leu Arg Arg Trp Gly Ala 20

<210> 398

<211> 26

<212> PRT

<213> Homo sapiens

<400> 398

Ser Glu Lys Glu Gly Lys Asp Phe Ser Gly Phe Ala Leu Ser Ile His 5

Gly Pro Glu Arg Lys Lys Glu Glu Gly Trp 20

<210> 399

<211> 86

<212> PRT

```
WO 99/31117
                                     195
 <213> Homo sapiens
<400> 399
Met Asn Glu Cys Ile Ala Lys Pro Cys Met Ala Ala Phe Cys Ser Cys
Pro Ser Cys Cys Leu Pro Ser Arg Pro Gly Cys Ser Arg Glu Gln Arg
                                 25
Cys Ala Phe Ser Cys Glu Pro Cys His Thr Val Glu His Trp Val Glu
Pro Met Gly Gln Gly Gln Arg Gln Glu His Thr Gln Gly Ser Val Leu
Pro Ser Ser His Pro Ser Arg Gly Lys Ala Thr Thr Val His Ser Cys
Cys Gln Glu Pro Trp Gly
<210> 400
<211> 27
<212> PRT
<213> Homo sapiens
<400> 400
Phe Cys Ser Cys Pro Ser Cys Cys Leu Pro Ser Arg Pro Gly Cys Ser
```

Arg Glu Gln Arg Cys Ala Phe Ser Cys Glu Pro 20

<210> 401 <211> 23 <212> PRT <213> Homo sapiens <400> 401 Gly Gln Arg Gln Glu His Thr Gln Gly Ser Val Leu Pro Ser Ser His Pro Ser Arg Gly Lys Ala Thr

<210> 402 <211> 139 <212> PRT <213> Homo sapiens <400> 402 Gly Val Val Asn Ser Cys Leu Leu Pro Leu Pro Pro Arg Leu Leu Ala

5

20

196

Thr Gly Met Asp Cys Gly Gly Phe Ala Ser Arg Arg Met Gly Gly Arg 20 25 30

Gln His Ala Ala Leu Ser Val Phe Leu Pro Leu Pro Leu Ala His Gly $35 \hspace{1cm} 40 \hspace{1cm} 45$

Leu Tyr Pro Met Phe Asn Cys Val Ala Gly Leu Thr Gly Lys Gly Thr 50 60

Ser Leu Leu Ser Gly Ala Ala Arg Pro Ala Gly Glu Ala Ala Arg 65 70 75 80

Ala Gly Thr Lys Gly Ser His Ala Arg Phe Gly Asn Ala Phe Ile His 85 90 95

Ser Phe Ile His Ser Phe Ile Glu Cys Leu Leu Asn Thr Tyr Cys Val 100 105 110

Pro Ser Ser Ala Leu Thr Ala Val Gly Ile Gly Asp Ile Leu Lys Asn 115 120 125

Lys Asn Asp Lys Ser Ser Cys Leu Cys Ser Cys 130 135

<210> 403

<211> 25

<212> PRT

<213> Homo sapiens

<400> 403

Gly Met Asp Cys Gly Gly Phe Ala Ser Arg Arg Met Gly Gly Arg Gln

1 5 10 15

His Ala Ala Leu Ser Val Phe Leu Pro 20 25

<210> 404

<211> 25

<212> PRT

<213> Homo sapiens

<400> 404

Leu Thr Gly Lys Gly Thr Ser Leu Leu Ser Gly Ala Ala Arg Pro Ala 1 5 10 15

Gly Glu Ala Ala Ala Arg Ala Gly Thr
20 25

<210> 405

<211> 22

<212> PRT

<213> Homo sapiens

<400> 405

197

Leu Asn Thr Tyr Cys Val Pro Ser Ser Ala Leu Thr Ala Val Gly Ile $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Gly Asp Ile Leu Lys Asn 20

<210> 406

<211> 55

<212> PRT

<213> Homo sapiens

<400> 406

Thr Ser Leu Ser Gln Leu Trp His Phe Cys His Phe Trp Pro Val Lys

1 5 10 15

Phe Cys Cys Gly Gly Cys Pro Val His Cys Arg Met Phe Ser Ser Ile
20 25 30

Ser Gly Leu Tyr Leu Leu Asn Ala Ser Ala Pro Ser Leu Gln Leu Asn 35 40 45

Asp Pro Lys Cys Leu Gln Thr 50 55

<210> 407

<211> 28

<212> PRT

<213> Homo sapiens

<400> 407

Trp Pro Val Lys Phe Cys Cys Gly Gly Cys Pro Val His Cys Arg Met

1 5 10 15

Phe Ser Ser Ile Ser Gly Leu Tyr Leu Leu Asn Ala 20 25

<210> 408

<211> 20

<212> PRT

<213> Homo sapiens

<400> 408

Ser Cys Arg Cys Trp Ala Leu Gly Ala Gly Gly Gly Gln Arg Gln Trp

1 5 10 15

Val Gly Arg Ser

20

<210> 409

<211> 80

<212> PRT

<213> Homo sapiens

<400> 409

Thr Gly Ala Gln Ala Pro Lys Met Gly Ala Arg Gln Arg Lys Arg Pro 1 5 10 15

Leu Gln Thr Arg Ile Lys Asn Ser Ser Lys Ser Thr Leu Trp Pro Pro 20 25 30

Gln Trp Val Arg Cys Gly Arg Trp Trp Thr Trp Pro Ser Arg Lys Lys
35 40 45

Thr Ser Arg Pro Arg Arg Gln Leu Phe Thr Ser Thr Leu Ser Thr Ser 50 55 60

Ala Ser Ala Leu Val Trp Pro Val Ser Trp Phe Ser Gln Glu Gly His
65 70 75 80

<210> 410

<211> 25

<212> PRT

<213> Homo sapiens

<400> 410

Met Gly Ala Arg Gln Arg Lys Arg Pro Leu Gln Thr Arg Ile Lys Asn $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Ser Ser Lys Ser Thr Leu Trp Pro Pro 20 25

<210> 411

<211> 23

<212> PRT

<213> Homo sapiens

<400> 411

Pro Arg Arg Gln Leu Phe Thr Ser Thr Leu Ser Thr Ser Ala Ser Ala 1 5 10 15

Leu Val Trp Pro Val Ser Trp
20

<210> 412

<211> 25

<212> PRT

<213> Homo sapiens

<400> 412

Asp Gly Gly Lys Glu Glu Gly Val Ser Cys Leu Lys Ile Ser Leu

1 5 10 15

Leu Cys Gly Pro Trp Leu Trp Leu Pro 20 25

```
<210> 413
  <211> 135
  <212> PRT
  <213> Homo sapiens
  <400> 413
  His Glu Met Gly Glu Leu Ala Ile Cys His Thr Arg Val Pro Phe Ser
  Leu Pro Ser Ser Ala Gln Gly Val Pro Gln Asn Leu Gln Gly Pro Ile
  Gly His Leu Ala Val Cys Thr Pro Ser Ser Leu Thr Ser Trp His Phe
                               40
  Pro Gln Lys Arg Glu Lys Trp Ser Thr Val Asn Lys Arg Gln Arg Phe
 Leu Gln Phe Pro Ala Pro Leu Arg Asn Trp Ile Pro Gln Thr Pro Leu
 Ser Leu Ser Val Ser Ser Gly Pro Leu Gly Ser Phe Thr Val Phe Thr
 Leu Leu Ser Leu Cys Ala Trp Pro Trp Cys Cys Arg Asp Cys Tyr Lys
                                 105
 Ser Cys Cys Pro Ile Pro Ile Phe Asn Leu Thr Ala Pro Leu Cys Val
 His Thr Pro Glu Pro Ser Ser .
     130
                         135
<210> 414
<211> 23
<212> PRT
<213> Homo sapiens
<400> 414
Ser Ser Ala Gln Gly Val Pro Gln Asn Leu Gln Gly Pro Ile Gly His
                 - 5
Leu Ala Val Cys Thr Pro Ser
             20
<210> 415
<211> 28
<212> PRT
<213> Homo sapiens
<400> 415
```

SUBSTITUTE SHEET (RULE 26)

Val Asn Lys Arg Gln Arg Phe Leu Gln Phe Pro Ala Pro Leu Arg Asn

Trp Ile Pro Gln Thr Pro Leu Ser Leu Ser Val Ser 20 25

<210> 416

<211> 23

<212> PRT

<213> Homo sapiens

<400> 416

Cys Cys Arg Asp Cys Tyr Lys Ser Cys Cys Pro Ile Pro Ile Phe Asn
1 5 10 15

Leu Thr Ala Pro Leu Cys Val 20

<210> 417

<211> 150

<212> PRT

<213> Homo sapiens

<400> 417

Asp Leu Asn Val Thr Asn Glu Gly Glu Gly Lys Glu Val Leu Gly Gln
1 5 10 15

Gly Ser Thr Asn Asn Glu Lys Lys Cys Gln Lys Ala Thr Ser Asn Thr 20 25 30

Glu Pro Arg Ala Arg Glu Ala Lys Ala Arg His Ala Asn Met Gly Thr
35 40 45

Ser Asp Arg Glu Ser Pro Thr Trp Ser Leu Thr Ala Glu Gly Leu Lys
50 55 60

Ala Lys Ser Lys Met Gln Gly Lys Ala Thr Lys Gly Ala Ala Ser Thr 65 70 75 80

Met Gly Ser His Asn Gln Gly Pro His Lys Arg Glu Ile Phe Lys His 85 90 95

Glu Thr Pro Ser Ser Phe Pro Pro Pro Ser Gln Cys Gln Pro Glu Leu 100 105 110

Leu Pro Tyr Lys Tyr Trp Ala Thr Leu Ala Ser Gly Tyr Val Pro Ser 115 120 125

Trp Leu Pro Ser Val Asp Ser Tyr Arg Ile Asn Thr Ala Ile Lys Asp 130 135 140

Lys Asn Gly Gln Asp Thr 145 150

<210> 418 <211> 24

<212> PRT

<213> Homo sapiens

<400> 418

Val Leu Gly Gln Gly Ser Thr Asn Asn Glu Lys Lys Cys Gln Lys Ala 10

Thr Ser Asn Thr Glu Pro Arg Ala 20

<210> 419

<211> 29

<212> PRT

<213> Homo sapiens

<400> 419

Arg Glu Ser Pro Thr Trp Ser Leu Thr Ala Glu Gly Leu Lys Ala Lys 1 5

Ser Lys Met Gln Gly Lys Ala Thr Lys Gly Ala Ala Ser

<210> 420

<211> 22

<212> PRT

<213> Homo sapiens

<400> 420

Gly Tyr Val Pro Ser Trp Leu Pro Ser Val Asp Ser Tyr Arg Ile Asn 5

Thr Ala Ile Lys Asp Lys 20

<210> 421

<211> 12

<212> PRT

<213> Homo sapiens

<400> 421

Asn Ser Ala Glu Gln Ser Met Leu Ile Leu Val Thr 5

<210> 422

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 422

Arg Xaa Asp Arg Xaa Pro Val Pro Glu Leu Pro Gly Tyr Glu Pro Thr

Arg Thr Asp Ile Ser Ser Phe Lys Asn Ile Tyr Arg Tyr Ala Phe Asp

Phe Ala Arg Asp Lys Asp Gln Arg Ser Leu Asp Ile Asp Thr Ala Lys

Ser Met Leu Ala Leu Leu Gly Arg Thr Trp Pro Leu Phe Ser Val 60

Phe Tyr Gln Tyr Leu Glu Gln Ser Lys Tyr Arg Val Met Asn Lys Asp

Gln Trp Tyr Asn Val Leu Glu Phe Ser Arg Thr Val His Ala Asp Leu

Ser Asn Tyr Asp Glu Asp Gly Ala Trp Pro Val Leu Leu Asp Glu Phe 105

Val Glu Trp Gln Lys Val Arg Gln Thr Ser

<210> 423

<211> 28

<212> PRT

<213> Homo sapiens

<400> 423

Pro Thr Arg Thr Asp Ile Ser Ser Phe Lys Asn Ile Tyr Arg Tyr Ala

Phe Asp Phe Ala Arg Asp Lys Asp Gln Arg Ser Leu

<210> 424

<211> 29

<212> PRT

<213> Homo sapiens

<400> 424

Ser Met Leu Ala Leu Leu Gly Arg Thr Trp Pro Leu Phe Ser Val

Phe Tyr Gln Tyr Leu Glu Gln Ser Lys Tyr Arg Val Met

```
<210> 425
 <211> 27
 <212> PRT
                                                     <213> Homo sapiens
 <400> 425
 Phe Ser Arg Thr Val His Ala Asp Leu Ser Asn Tyr Asp Glu Asp Gly
                                    10
 Ala Trp Pro Val Leu Leu Asp Glu Phe Val Glu
              20
 <210> 426
 <211> 10
 <212> PRT
 <213> Homo sapiens
 <400> 426
 Ile Tyr Arg Tyr Ala Phe Asp Phe Ala Arg
         5
 <210> 427
 <211> 8
 <212> PRT
 <213> Homo sapiens
 <400> 427
Lys Asp Gln Arg Ser Leu Asp Ile
<210> 428
<211> 8
<212> PRT
<213> Homo sapiens
<400> 428
Asn Val Leu Glu Phe Ser Arg Thr
            5
<210> 429
<211> 21
<212> PRT
<213> Homo sapiens
<400> 429
Asp Leu Ser Asn Tyr Asp Glu Asp Gly Ala Trp Pro Val Leu Leu Asp
Glu Phe Val Glu Trp
            20
<210> 430
```

<211> 37

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (15)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 430

Leu Phe Arg Cys Pro Ile Gly Lys Ala Gly Thr Pro Ala Gly Xaa Gly 1 5 10 15

Pro Glu Phe Pro Gly Arg Pro Thr Arg Pro Val Arg Glu Lys Glu Leu 20 25 30

Thr Glu Thr Phe Glu 35

<210> 431

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (9)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 431

Gly Lys Ala Gly Thr Pro Ala Gly Xaa Gly Pro Glu Phe Pro Gly Arg
1 5 10 15

Pro Thr Arg Pro Val

<210> 432

<211> 45

<212> PRT

<213> Homo sapiens

<400> 432

Phe Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
1 5 10 15

Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile 20 25 30

Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
35 40 45

<210> 433

<211> 21

<212> PRT

<213> Homo sapiens

<400> 433

Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro 10

Thr Thr Pro Leu Pro 20

<210> 434

<211> 61

<212> PRT

<213> Homo sapiens

<400> 434

Phe Tyr Pro Pro Met Thr Gln Gly Lys Glu Ser Leu Pro Leu Leu Ala 10

Leu Gln Ile Phe Asn Thr Thr Phe Arg Pro Ser Phe Ala Phe Phe Ser 20 25

Gly His Arg Thr Leu Phe Phe Gly Val Arg Ser Pro Asn Pro Pro Lys

Pro Arg Ile Phe Leu Ile Trp Leu Ile Ala Val Ala Leu 55

<210> 435

<211> 31

<212> PRT

<213> Homo sapiens

<400> 435

Leu Leu Ala Leu Gln Ile Phe Asn Thr Thr Phe Arg Pro Ser Phe Ala

Phe Phe Ser Gly His Arg Thr Leu Phe Phe Gly Val Arg Ser Pro 25

<210> 436

<211> 52

<212> PRT

<213> Homo sapiens

<400> 436

His Leu Ala Gln Thr Val Met Met His Pro Gln Lys Ser Phe Tyr Gln

Val Lys Asn Thr Asn His Ser Asp Arg Gly Ala Ile Glu Glu Thr Gln

Ile Leu Glu Asp Arg Leu Gly Gln Ile Pro Leu Cys Leu Glu Ser Gln 40

Ile Trp Glu Ala 50 <210> 437 <211> 28 <212> PRT <213> Homo sapiens <400> 437 Lys Asn Thr Asn His Ser Asp Arg Gly Ala Ile Glu Glu Thr Gln Ile Leu Glu Asp Arg Leu Gly Gln Ile Pro Leu Cys Leu <210> 438 <211> 73 <212> PRT <213> Homo sapiens <400> 438 Gln Gly Cys Tyr Arg Arg Asp Ser Asn Ile Gly Arg Gln Val Arg Pro Asp Ser Ile Met Leu Arg Lys Pro Asp Leu Gly Ser Ile Thr His Tyr Gly Ser Val Leu Gly Asn Leu Asn Tyr Cys Asp Leu Pro Gln Leu Tyr Arg Asn Pro Ser Leu Gly Asn Ser Gly Met Arg Glu Met Phe Ser Pro 55 Phe Tyr Asn Pro Val Glu Cys His Pro 65 70 <210> 439 <211> 23 <212> PRT <213> Homo sapiens <400> 439 Pro Asp Ser Ile Met Leu Arg Lys Pro Asp Leu Gly Ser Ile Thr His Tyr Gly Ser Val Leu Gly Asn 20 <210> 440 <211> 22 <212> PRT

<213> Homo sapiens

<400> 440

Tyr Arg Asn Pro Ser Leu Gly Asn Ser Gly Met Arg Glu Met Phe Ser

Pro Phe Tyr Asn Pro Val 20

<210> 441

<211> 21

<212> PRT

<213> Homo sapiens

<400> 441

Asn Ser Ala Arg Gly Leu Ser Gly Gly His Pro Phe Pro Trp Leu Ser

Glu Gly His Pro Phe 20

<210> 442

<211> 107

<212> PRT

<213> Homo sapiens

<400> 442

Thr Asp Ser Asp Leu Thr Leu Gly Ile Leu Leu Gly Ile Tyr Thr

Asn His Ile Trp Glu Met Phe Leu Ala Ala Ser Arg Ile Asn Ser Pro 20

Lys Leu Glu Pro Glu Lys Ser Val Lys Arg Gln Ile Asn Phe Pro Ser

Ser Lys Asp Val Gly Cys Ser Leu Glu Val Pro Lys Asp Gly Pro Pro 50

Leu Ser His Gly Lys Glu Trp Ile Pro Leu Ser His Arg Lys Gly Trp

Tile Pro Leu Ser His Met Lys Gly Trp Pro Ser Leu Ser His Gly Lys

Gly Trp Pro Pro Leu Ser Pro Arg Ala Glu Phe 100 105

<210> 443

<211> 20

<212> PRT

<213> Homo sapiens

<400> 443

Leu Gly Ile Leu Leu Gly Ile Tyr Thr Asn His Ile Trp Glu Met 5

```
Phe Leu Ala Ala
             20
<210> 444
<211> 27
<212> PRT
<213> Homo sapiens
<400> 444
Lys Ser Val Lys Arg Gln Ile Asn Phe Pro Ser Ser Lys Asp Val Gly
Cys Ser Leu Glu Val Pro Lys Asp Gly Pro Pro
         . 20
                                 25
<210> 445
<211> 27
<212> PRT
<213> Homo sapiens
Gly Lys Glu Trp Ile Pro Leu Ser His Arg Lys Gly Trp Ile Pro Leu
                 5
Ser His Met Lys Gly Trp Pro Ser Leu Ser His
             20
<210> 446
<211> 47
<212> PRT
<213> Homo sapiens
<400> 446
Gly Trp Ala Ser Thr Gln Pro Arg Glu Arg Met Asp Pro Ala Gln Pro
                5
Gln Glu Arg Met Asp Pro Ser Gln Pro His Glu Arg Met Ala Leu Thr
                                 25
Gln Pro Trp Lys Arg Met Ala Pro Thr Gln Pro Ser Cys Arg Ile
<210> 447
<211> 24
<212> PRT
<213> Homo sapiens
<400> 447
Pro Ala Gln Pro Gln Glu Arg Met Asp Pro Ser Gln Pro His Glu Arg
Met Ala Leu Thr Gln Pro Trp Lys
```

<210> 448 <211> 30

<212> PRT

<213> Homo sapiens

<400> 448

Ile Ala Asn Gly Gly Gly Arg Pro Ile Lys Leu Asn Ala Leu Tyr Lys

1 5 10 15

Ile Gln Asn Glu Cys Lys Ile Val Phe Thr Cys Ile Asp Phe 20 25 30

<210> 449

<211> 33

<212> PRT

<213> Homo sapiens

<400> 449

Met Pro Cys Ile Lys Ser Lys Met Asn Ala Lys Leu Phe Ser Leu Val 1 5 10 15

Leu Thr Leu Cys Cys Met Ile Pro Ile Ser Val Leu Phe Gly Thr Cys
20 25 30

Ile

<210> 450

<211> 101

<212> PRT

<213> Homo sapiens

<400> 450

Gln Val Ala Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser 1 5 10 15

Cys Phe Arg Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr
20 25 30

Arg Ser Ser Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln
35 40 45

Glu Ser Pro Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His 50 60

Lys Pro Thr Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe 65 70 75 80

Lys Lys Glu Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp 85 90 95

Ala Ala Lys Asn Lys

100 <210> 451 <211> 25 <212> PRT <213> Homo sapiens <400> 451 Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp 10 Val Ser Ser Ser Leu Arg Leu Thr Arg 20 <210> 452 <211> 20 <212> PRT <213> Homo sapiens <400> 452 Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr Asp 10 Trp Gln Lys Lys <210> 453 <211> 23 <212> PRT <213> Homo sapiens <400> 453

Ile Trp Ser Gly Arg Phe Lys Lys Glu Asp Glu Ile Pro Glu Thr Val 10

Ser Leu Glu Met Leu Asp Ala 20

<210> 454

<211> 63

<212> PRT

<213> Homo sapiens

<400> 454

Met Asp Phe Ala Gln Asn His Arg Lys Val Pro Glu Leu His Pro Ala

Leu Thr Thr Glu Cys Leu Tyr Thr Asn Leu Arg Ile Gly Arg Lys Arg 20 25

Ser Ser Tyr Gly Gln Val Ala Ser Lys Arg Lys Met Lys Ser Gln Arg 35

```
Leu Ser Arg Trp Arg Cys Leu Met Leu Gln Arg Thr Arg Cys Glu
                          55
 <210> 455
 <211> 19
 <212> PRT
 <213> Homo sapiens
<400> 455
Lys Val Pro Glu Leu His Pro Ala Leu Thr Thr Glu Cys Leu Tyr Thr
Asn Leu Arg
<210> 456
<211> 26
<212> PRT
<213> Homo sapiens
<400> 456
Lys Arg Ser Ser Tyr Gly Gln Val Ala Ser Lys Arg Lys Met Lys Ser
Gln Arg Leu Ser Arg Trp Arg Cys Leu Met
             20
<210> 457
<211> 12
<212> PRT
<213> Homo sapiens
<400> 457
Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
 1 5
<210> 458
<211> 9
<212> PRT
<213> Homo sapiens
<400> 458
Arg Val Pro Leu His Lys Pro Thr Asp
<210> 459
<211> 8
<212> PRT
<213> Homo sapiens
<400> 459
Trp Ser Gly Arg Phe Lys Lys Glu
```

212 <210> 460 <211> 9 <212> PRT <213> Homo sapiens <400> 460 Glu Met Leu Asp Ala Ala Lys Asn Lys <210> 461 <211> 9 <212> PRT <213> Homo sapiens <400> 461 Ser Tyr Leu Met Ile Ala Leu Thr Val 1 5 <210> 462 <211> 9 <212> PRT <213> Homo sapiens <400> 462 Met Val Ile Glu Gly Lys Lys Ala Ala 5 <210> 463 <211> 68 <212> PRT <213> Homo sapiens <400> 463 Arg Pro Gly Met Arg Ala Leu Gly Ser Cys Leu Ser Leu Leu Ala Leu 5 Cys Ser Pro Gln Ala Arg Pro Gly Pro Arg Thr Leu Asp Ala Ser Thr Ala Thr Leu Thr Pro His Phe Ser Pro Cys Ala Arg Phe Ser Pro Val 40 Gly Pro Ser Ala Val Pro Phe Ala Ala Thr Pro Leu Pro Leu Ala Gly 50 Pro His Gln Pro

SUBSTITUTE SHEET (RULE 26)

65

<210> 464 <211> 20

PCT/US98/27059

<212> PRT

<213> Homo sapiens

<400> 464

Gly Ser Cys Leu Ser Leu Leu Ala Leu Cys Ser Pro Gln Ala Arg Pro 1 5 10 15

Gly Pro Arg Thr

20

<210> 465

<211> 23

<212> PRT

<213> Homo sapiens

<400> 465

His Phe Ser Pro Cys Ala Arg Phe Ser Pro Val Gly Pro Ser Ala Val

1 5 10 15

Pro Phe Ala Ala Thr Pro Leu 20

<210> 466

<211> 92

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (43)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (80)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 466

Ala Ile Glu Glu Arg Asn Lys Ser Arg Leu Thr Gln Gln Ala Ser Glu

1 5 10 15

Pro Thr Gly Ser Pro Arg Tyr Leu His Glu Gln His Pro Gly Ser Arg

Ser Gln Met Asp Cys Gly Ser Leu Thr Met Xaa Cys Pro Pro Pro Arg
35 40 45

Val Arg Asp Asp Arg Thr Ser Ala Arg Gly Val Pro Arg Gln Ala Ala
50 55 60

Pro Asp Ile Val Gly Gly Arg Pro Ser Ser Arg Ala Cys Val Ser Xaa 65 70 75 80

Pro Ala Cys Ala Pro Ser Ala Ala Val Phe Pro Tyr

```
<210> 467
<211> 24
<212> PRT
<213> Homo sapiens
<400> 467
Leu Thr Gln Gln Ala Ser Glu Pro Thr Gly Ser Pro Arg Tyr Leu His
 1 5 10
Glu Gln His Pro Gly Ser Arg Ser
           20
<210> 468
<211> 25
<212> PRT
<213> Homo sapiens
<400> 468
Ser Ala Arg Gly Val Pro Arg Gln Ala Ala Pro Asp Ile Val Gly Gly
                   10
Arg Pro Ser Ser Arg Ala Cys Val Ser
          20
<210> 469
<211> 14
<212> PRT
<213> Homo sapiens
<400> 469
Pro Arg Val Arg Lys Thr Pro His Leu Ser Ala Ser Gly Lys
<210> 470
<211> 59
<212> PRT
<213> Homo sapiens
<400> 470
Tyr Tyr Tyr Ser Met Leu Lys Ile Cys His Ile Thr Ile Leu Glu Thr
Leu Ser Asp Arg Thr Pro Arg Lys Phe Ala Lys Lys Cys Tyr Ile Leu
                             25
Tyr Ile Lys Leu Ser Asp Ser Ser Val Glu Lys Val Ala Tyr Thr Leu
        35
Leu Leu Ile Pro Ala Ala Ile Glu Lys Lys
    50
                      55
```

<210> 471

<211> 32

<212> PRT

<213> Homo sapiens

<400> 471

Thr Ile Leu Glu Thr Leu Ser Asp Arg Thr Pro Arg Lys Phe Ala Lys

1 5 10 15

PCT/US98/27059

Lys Cys Tyr Ile Leu Tyr Ile Lys Leu Ser Asp Ser Ser Val Glu Lys
20 25 30

<210> 472

<211> 17

<212> PRT

<213> Homo sapiens

<400> 472

Val His Thr Lys Glu Ile Phe Arg Glu Arg Ser Ala Gly Phe Pro Val 1 5 10 15

Lys

<210> 473

<211> 97

<212> PRT

<213> Homo sapiens

<400> 473

Leu Glu Met Gly Phe Gln Pro Thr Lys Glu Ile Asn Ala Arg Gly Ser 1 5 10 15

Glu Pro Cys Gln Ala Gln Ser Thr Ser Leu Pro Lys Leu Pro Arg Trp
20 25 30

Gly Ser Arg Pro Glu Ala Pro Gln Thr Pro Gln Gly Gly Leu Glu Ser 35 40 45

Arg Cys Cys Thr Pro Val Ser Lys Gln Ser Leu Asn Leu Lys Ala Asp 50 55 60

Arg Phe Lys Ala Leu Thr Leu Gly Arg Ala Gln Trp Leu Thr Pro Val 65 70 75 80

Ile Gln Ala Leu Ser Glu Leu Arg Trp Val Asp His Leu Arg Ser Gly
85 90 95

Val

```
216
<210> 474
<211> 24
<212> PRT
<213> Homo sapiens
<400> 474
Phe Gln Pro Thr Lys Glu Ile Asn Ala Arg Gly Ser Glu Pro Cys Gln
Ala Gln Ser Thr Ser Leu Pro Lys
      . 20
<210> 475
<211> 27
<212> PRT
<213> Homo sapiens
<400> 475
Pro Lys Leu Pro Arg Trp Gly Ser Arg Pro Glu Ala Pro Gln Thr Pro
                  5
Gln Gly Gly Leu Glu Ser Arg Cys Cys Thr Pro
            20
<210> 476
<211> 27
<212> PRT
<213> Homo sapiens
<400> 476
Arg Phe Lys Ala Leu Thr Leu Gly Arg Ala Gln Trp Leu Thr Pro Val
1
       5
                                    10
Ile Gln Ala Leu Ser Glu Leu Arg Trp Val Asp
            20
<210> 477
<211> 176
<212> PRT
<213> Homo sapiens
<400> 477
Arg Ile Pro Leu Gln Ser Asp Gly Ser Phe Leu His Glu Lys Ser Ser
Gln Gln Arg Ser Asn Arg Asn Phe Pro Cys Pro Thr Leu Gln Cys Asn
                                25
```

SUBSTITUTE SHEET (RULE 26)

Pro Glu Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His

Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn

217

Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu 65 70 75 80

Lys Ile Pro Ser Thr Leu Ala Pro Pro Met Asp Pro Ser Val Pro Ile 85 90 95

Trp Ile Ile Ile Phe Gly Val Ile Phe Cys Ile Ile Ile Val Ala Ile
100 105 110

Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln Arg Arg Lys Asn Lys 115 120 125

Glu Pro Ser Glu Val Asp Asp Ala Glu Asp Lys Cys Glu Asn Met Ile 130 135 140

Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly 145 150 155 160

His Ile Asn Asp Ala Phe Met Thr Glu Asp Glu Arg Leu Thr Pro Leu 165 170 175

<210> 478

<211> 25

<212> PRT

<213> Homo sapiens

<400> 478

Pro Cys Pro Thr Leu Gln Cys Asn Pro Glu Val Ser Phe Trp Phe Val

1 5 10 15

Val Thr Asp Pro Ser Lys Asn His Thr

·<210> 479

<211> 23

<212> PRT

<213> Homo sapiens

<400> 479

Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn 1 5 10 15

Asp Gln Thr Leu Glu Phe Leu

<210> 480

<211> 24

<212> PRT

<213> Homo sapiens

<400> 480

218

Ile Trp Gln Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp Asp 1 5 10 15

Ala Glu Asp Lys Cys Glu Asn Met 20

<210> 481

<211> 19

<212> PRT

<213> Homo sapiens

<400> 481

Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu

1 10 15

Asp Glu Arg

<210> 482

<211> 136

<212> PRT

<213> Homo sapiens

<400> 482

Gly Ser Arg Thr Thr Ala Leu Gln Arg Gly Val Ser Leu Ser Ser 1 5 10 15

Val Met Lys Ala Ser Leu Ile Cys Pro Pro Phe Met Ser Arg Gly Ser
20 25 30

Glu Gly Met Pro Phe Ser Ile Val Ile Met Phe Ser His Leu Ser Ser 35 40 45

Ala Ser Ser Thr Ser Asp Gly Ser Leu Phe Phe Leu Leu Arg Cys Gln 50 55

Ile Pro Asp Lys Ile Ser Ser Ala Ile Ala Thr Met Met Gln Asn 65 70 75 80

Ile Thr Pro Asn Ile Ile Ile Gln Met Gly Thr Asp Gly Ser Met Gly 85 90 95

Gly Ala Ser Val Glu Gly Ile Phe Lys Asn Ser Arg Val Trp Ser Phe 100 105 110

Arg Lys Lys Ala Leu Leu Ile Arg Phe Leu Phe Ile Leu Met Ala Asp 115 120 125

Cys Thr Ser Thr Ala Gly Arg Val 130 135

<210> 483

<211> 28

<212> PRT

```
<213> Homo sapiens
```

<400> 483

Val Ser Leu Ser Ser Ser Val Met Lys Ala Ser Leu Ile Cys Pro Pro 1 5 10 15

Phe Met Ser Arg Gly Ser Glu Gly Met Pro Phe Ser 20 25

<210> 484

<211> 24

<212> PRT

<213> Homo sapiens

<400> 484

Ser Met Gly Gly Ala Ser Val Glu Gly Ile Phe Lys Asn Ser Arg Val 1 5 10 15

Trp Ser Phe Arg Lys Lys Ala Leu 20

<210> 485

<211> 29

<212> PRT

<213> Homo sapiens

<400> 485

Gly Ala Arg Gly Ser Gln Gln Asp Ala Pro Ala Leu Gln Glu Ala Glu

1 5 10 15

Val Arg Gly Pro Glu Arg Ala Gln Pro Ala Arg Gly Arg

<210> 486

<211> 439

<212> PRT

<213> Homo sapiens

<400> 486

Ser Glu Arg Pro Gly Glu Gly Pro Ala Arg Pro Gly Gln Asp Asp Gln 1 5 10 15

Gly Pro Ala Val Pro Ala Val Ala Gly Ala Gly Val Gly Val His Asp

Pro Ala Asp His Arg Val Leu Gly Gln Arg Ser Ala Ala His Phe Tyr 35 40 45

Leu His Thr Ser Phe Ser Arg Pro His Thr Gly Pro Pro Leu Pro Thr 50 55 60

Pro Gly Pro Asp Arg Thr Gly Ser Ser Arg Pro Thr Pro Met Ser Thr 65 70 75 80

Ser	Phe	Trp	Thr	Ile	Ser	His	Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro
				85					90					95	

- Arg Lys Glu Thr Glu Gln Pro Pro Ala Pro Gly Glu His Gly Glu 100 105 110
- Arg Glu Arg Leu Arg Leu Val Pro Ala Arg Arg Pro Ala Gln Pro Arg 115 120 125
- Pro Gly Pro Ala Ala Gly Gly Ala Glu Glu Arg Ala Ala Gly Leu Leu 130 135 140
- Arg Gln Leu Gln Pro Gly Leu Pro His Gln Gly Ala Arg Ile Arg Arg 145 150 155 160
- His Pro Gln Leu Gly Ala Glu Pro Pro Asp Arg Gly Arg Pro Ala Arg 165 170 175
- Gly His Leu Leu Arg Ala Gln Gly Gly Leu His Gln Leu Glu Ala 180 185 190
- Arg Asp Asp Arg Ala Glu Arg Lys Pro Ala Ala Pro Arg Cys Ala Leu 195 200 205
- Pro Arg Pro Ala Ala His Pro Ala Arg Ala Arg Ala Gln Arg Gln Arg 210 215 220
- Ala Pro Asp Leu Gln Gln Val Leu Ala Pro Leu Arg Glu Ala Leu Pro 225 230 235 240
- Pro Pro His Glu Gly Gln Ala Gln Glu Val His Gln Val Pro Leu Arg
 245 250 255
- Ala Arg Pro Leu Arg Ala Pro Asp Leu Arg Leu Pro Gln Gln Val Arg 260 265 270
- Ala Gly Glu Arg Gly Val Leu Pro Gln Val Arg Arg Ala His Ala Ala 275 280 285
- Gly Val Arg Gln Pro His Gln Pro Ala Arg Leu Gly Ala Arg Gly Leu 290 295 300
- Pro Arg Trp Pro Gln Gly Val Leu Arg Gln Leu His Pro Val Pro Ala 305 310 315 320
- Gly Pro Ala His Gly Glu Ala Gly Ala Leu Gln Arg Ala Leu Ala Ala 325 330 335
- Gly Val Pro Pro Leu Pro Pro Val Pro Asp Arg Leu Arg Phe Leu Gly 340 345 350
- Lys Leu Glu Thr Leu Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu 355 360 365
- Gln Val Asp Arg Gln Ser Ala Ser Pro Arg Ala Thr Gly Thr Gly Pro 370 375 380

221

Pro Ala Ala Gly Arg Arg Thr Gly Ser Pro Arg Ser Pro Trp Pro Gly 385 390 395 400

Gly Ser Ser Cys Ile Asn Ser Thr Arg Pro Thr Leu Phe Ser Ser Ala
405 410 415

Thr Pro Ser Pro Lys Thr Ser Ser Glu Thr Glu Ser Phe Arg Val Ala 420 425 430

Phe Ser Arg Val Pro Gly Thr 435

<210> 487

<211> 25

<212> PRT

<213> Homo sapiens

<400> 487

Arg Pro Gly Gln Asp Asp Gln Gly Pro Ala Val Pro Ala Val Ala Gly
1 5 10 15

Ala Gly Val Gly Val His Asp Pro Ala
20 25

<210> 488

<211> 21

<212> PRT

<213> Homo sapiens

<400> 488

Ser Arg Pro His Thr Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg

1 5 10 15

Thr Gly Ser Ser Arg 20

<210> 489

<211> 23

<212> PRT

<213> Homo sapiens

<400> 489

Ser His Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu

1 5 10 15

Gln Pro Pro Ala Pro Gly Glu 20

<210> 490

<211> 23

<212> PRT

<213> Homo sapiens

222

<400> 490

Arg Arg Pro Ala Gln Pro Arg Pro Gly Pro Ala Ala Gly Gly Ala Glu

1 5 10 15

Glu Arg Ala Ala Gly Leu Leu 20

<210> 491

<211> 23

<212> PRT

<213> Homo sapiens

<400> 491

Arg Arg His Pro Gln Leu Gly Ala Glu Pro Pro Asp Arg Gly Arg Pro

1 5 10 15

Ala Arg Gly His Leu Leu Leu 20

<210> 492

<211> 25

<212> PRT

<213> Homo sapiens

<400> 492

Arg Asp Asp Arg Ala Glu Arg Lys Pro Ala Ala Pro Arg Cys Ala Leu 1 5 10 15

Pro Arg Pro Ala Ala His Pro Ala Arg 20 25

<210> 493

<211> 27

<212> PRT

<213> Homo sapiens

<400> 493

Arg Ala Pro Asp Leu Gln Gln Val Leu Ala Pro Leu Arg Glu Ala Leu

1 5 10 15

Pro Pro Pro His Glu Gly Gln Ala Gln Glu Val 20 25

<210> 494

<211> 26

<212> PRT

<213> Homo sapiens

<400> 494

Asp Leu Arg Leu Pro Gln Gln Val Arg Ala Gly Glu Arg Gly Val Leu

1 10 15

Pro Gln Val Arg Arg Ala His Ala Ala Gly

20

25

<210> 495 <211> 27

<212> PRT

<213> Homo sapiens

<400> 495

Gln Pro Ala Arg Leu Gly Ala Arg Gly Leu Pro Arg Trp Pro Gln Gly
1 5 10 15

Val Leu Arg Gln Leu His Pro Val Pro Ala Gly
20 25

<210> 496

<211> 24

<212> PRT

<213> Homo sapiens

<400> 496

Ala Gly Val Pro Pro Leu Pro Pro Val Pro Asp Arg Leu Arg Phe Leu

1 5 10 15

Gly Lys Leu Glu Thr Leu Asp Glu

<210> 497

<211> 25

<212> PRT

<213> Homo sapiens

<400> 497

Gln Leu Leu Gln Leu Leu Gln Val Asp Arg Gln Ser Ala Ser Pro Arg

1 5 10 15

Ala Thr Gly Thr Gly Pro Pro Ala Ala

<210> 498

<211> 25

<212> PRT

<213> Homo sapiens

<400> 498

Asn Ser Thr Arg Pro Thr Leu Phe Ser Ser Ala Thr Pro Ser Pro Lys

1 10 15

Thr Ser Ser Glu Thr Glu Ser Phe Arg
20 25

<210> 499

<211> 324

<212> PRT

<213> Homo sapiens

<400> 499

Leu Gly Gly Lys Arg Thr Ala Gly Pro Pro Gly Val Ala Ala Ala Ala 1 5 10 15

Ala Arg Arg Pro Arg Pro Glu Ser Pro Ala Ser Pro Gly Ile Val Val 20 25 30

Asp Leu Ala Arg Val Ala Glu Ala Val His Leu Pro Pro Val Leu Val 35 40 45

Glu Gly Arg Gln Leu Leu Arg Val Arg Val Gln Gln Val Leu Asp Glu 50 55 60

Val Gly Glu Gly His Leu Glu Ala Ser Ala Glu Gly Leu Ala Arg Arg 65 70 75 80

Gly Gly Gln Ala Gly Val Val Gly Val His Pro Gln His Gly His Gly 85 90 95

Glu Leu Ala Val Glu Leu Leu Val Leu Gln Leu Glu Leu Ala Ala Glu 100 105 110

Gly Gly Asp Gln Ala His Glu Gly Val Ala His Glu Glu Glu Leu Gly
115 120 125

Val Leu Leu Glu Leu Asp Leu His Glu Val Ala Gly Glu Leu Pro Val 130 135 140

Ala Ala Pro Glu Leu Val Glu Gly Gln Val Arg Ala Gly Val Val His 145 150 155 160

Val Leu Ala Arg Asp Ala Gln Arg Val Ala Val Gly Arg Thr Ala Val
165 170 175

Gln Gln Ala Ser Ala Gln His Asp His His Ala Leu Pro Val Gly Ala 180 185 190

Gly His Leu Gly His Val Ala Val Asp Gly Pro Val Pro Val Val His 195 200 205

Asp Gln Val Ala Gln Leu Arg Val Gly Asp Val Val Glu Cys Ala Leu 210 215 220

Leu Gly Gly Glu Gly Gln Ala Gly Val Gly Ala Glu Ala Pro Gln His 225 235 240

Val Pro Pro Leu Arg Leu Leu Pro Ala Leu Val Trp Ala Ala Pro Gly 245 250 255

Val Ala Arg Gly Pro Val Val Ala Ser His Ala Leu Leu His Ala Pro 260 265 270

Pro Ala Gln Ala Ala Ala Pro Ser Pro Phe Trp Glu Gly His Ser Ala 275 280 285

```
225
  Ser Arg Gln His Glu Lys Leu Ser Arg Asn Ser Ser Thr Ser Glu Ser
      290
                          295
  Ala Val Ser Ser Leu Ser Cys Pro Ala Arg Ala Trp Ala Ala Ala Ala
                      310
                                          315
  Pro Cys Ala Ala
 <210> 500
 <211> 23
 <212> PRT
 <213> Homo sapiens
 <400> 500
 Glu Ala Val His Leu Pro Pro Val Leu Val Glu Gly Arg Gln Leu Leu
                  5
 Arg Val Arg Val Gln Gln Val
              20
 <210> 501
 <211> 24
 <212> PRT
 <213> Homo sapiens
<400> 501
Gly His Leu Glu Ala Ser Ala Glu Gly Leu Ala Arg Arg Gly Gly Gln
                  5
                                   10
Ala Gly Val Val Gly Val His Pro
             20
<210> 502
<211> 28
<212> PRT
<213> Homo sapiens
<400> 502
Gln Leu Glu Leu Ala Ala Glu Gly Gly Asp Gln Ala His Glu Gly Val
Ala His Glu Glu Glu Leu Gly Val Leu Leu Glu Leu
                                 25
```

<210> 503

<211> 27

<212> PRT

<213> Homo sapiens

<400> 503

Gly Glu Leu Pro Val Ala Ala Pro Glu Leu Val Glu Gly Gln Val Arg

226

5 10 15

Ala Gly Val Val His Val Leu Ala Arg Asp Ala 20

<210> 504

<211> 25

<212> PRT

<213> Homo sapiens

<400> 504

Ala Val Gln Gln Ala Ser Ala Gln His Asp His His Ala Leu Pro Val

Gly Ala Gly His Leu Gly His Val Ala 20

<210> 505

<211> 25

<212> PRT

<213> Homo sapiens

<400> 505

His Asp Gln Val Ala Gln Leu Arg Val Gly Asp Val Val Glu Cys Ala

Leu Leu Gly Gly Glu Gly Gln Ala Gly 20

<210> 506

<211> 23

<212> PRT

<213> Homo sapiens

<400> 506

Ala Leu Val Trp Ala Ala Pro Gly Val Ala Arg Gly Pro Val Val Ala

Ser His Ala Leu Leu His Ala 20

<210> 507

<211> 28

<212> PRT

<213> Homo sapiens

<400> 507

Pro Pro Ala Gln Ala Ala Ala Pro Ser Pro Phe Trp Glu Gly His Ser 5

Ala Ser Arg Gln His Glu Lys Leu Ser Arg Asn Ser

<210> 508

<211> 314

<212> PRT

<213> Homo sapiens

<400> 508

Ser Arg Val Thr Phe Pro Glu Arg Arg Arg Ser Ser Arg Leu Arg Arg 1 5 10 15

Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp Trp Ser Pro Arg Asp 20 25 30

Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln Gln Ala Glu Arg Arg Asn 35 40 45

Val Leu Arg Gly Phe Cys Ala Asn Ser Ser Leu Ala Phe Pro Thr Lys
50 55 60

Glu Arg Ala Phe Asp Asp Ile Pro Asn Ser Glu Leu Ser His Leu Ile
65 70 75 80

Val Asp Asp Arg His Gly Ala Ile Tyr Cys Tyr Val Pro Lys Val Ala 85 90 95

Cys Thr Asn Trp Lys Arg Val Met Ile Val Leu Ser Gly Ser Leu Leu 100 105 110

His Arg Gly Ala Pro Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His
115 120 125

Val His Asn Ala Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg

Tyr Gly Lys Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr 145 150 155 160

Thr Lys Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala 165 170 175

Phe Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe 180 185 190

Ala Val Pro Met Leu Arg Val Tyr Ala Asn His Thr Ser Leu Pro Ala 195 200 205

Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe Ala Asn 210 215 220

Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu Ala Pro Phe 230 235 240

Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His Pro Cys Gln Ile 245 250 255

Asp Tyr Asp Ser Trp Gly Ser Trp Arg Leu Trp Thr Arg Thr Pro Arg 260 265 270

```
Ser Cys Cys Ser Tyr Ser Arg Trp Thr Gly Ser Pro Leu Pro Pro Glu
                             280
 Leu Pro Glu Gln Asp Arg Gln Gln Leu Gly Gly Leu Val Arg Gln
     290
 Asp Pro Pro Gly Leu Glu Ala Ala Ala Val
 <210> 509
 <211> 26
 <212> PRT
 <213> Homo sapiens
 <400> 509
Arg Ser Pro Asp Gln Gly Arg Gln Gln Ala Glu Arg Arg Asn Val Leu
                   5
Arg Gly Phe Cys Ala Asn Ser Ser Leu Ala
              20
<210> 510
<211> 28
<212> PRT
<213> Homo sapiens
<400> 510
Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro Asn Ser Glu Leu Ser His
Leu Ile Val Asp Asp Arg His Gly Ala Ile Tyr Cys
<210> 511
<211> 23
<212> PRT
<213> Homo sapiens
Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys Leu Ser Arg His Leu Met
                  5
Lys Val Lys Leu Lys Lys Tyr
             20
<210> 512
<211> 24
<212> PRT
<213> Homo sapiens
<400> 512
Phe Val Arg Leu Ile Ser Ala Phe Arg Ser Lys Phe Glu Leu Glu Asn
```

. 229

10

15

Glu Glu Phe Tyr Arg Lys Phe Ala 20

<210> 513

<211> 26

1

<212> PRT

<213> Homo sapiens

<400> 513

Thr Ser Leu Pro Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys

1 5 10 15

Val Ser Phe Ala Asn Phe Ile Gln Tyr Leu 20 25

<210> 514

<211> 25

<212> PRT

<213> Homo sapiens

<400> 514

Ser Tyr Ser Arg Trp Thr Gly Ser Pro Leu Pro Pro Glu Leu Pro Glu 1 5 15

Gln Asp Arg Gln Gln Leu Gly Gly Gly 20 25

<210> 515

<211> 6

<212> PRT

<213> Homo sapiens

<400> 515

Ser Thr Gly Cys Ser Glu 1 5

<210> 516

<211> 146

<212> PRT

<213> Homo sapiens

<400> 516

Cys Leu Cys Leu Gly Cys Gly Leu Pro Glu Leu His Ser Tyr Leu Asp
1 5 10 15

Pro Gly Pro Tyr Leu Leu Val Tyr Pro Thr Leu Phe Trp Leu Cys Pro
20 25 30

Ser Ala Val Ser Pro Trp Ala Tyr Thr Cys Tyr Gln Leu Gly Leu Gly
35 40 45

230

Pro Gln Trp Gly Ala Ala Ala Leu Ser Phe Thr Val Asp Ala Ala Ile 50 55 60

Arg Val Trp Asp Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp Phe 65 70 75 80

Arg Gly Gly Val Thr Asn Cys Ser Gly Pro Gln Thr Ala Ala Lys 85 90 95

Ser Trp Leu Pro Leu Leu Gln Leu Ser Phe Glu Ser Gly Arg Pro Arg 100 105 110

Cys Gly Leu Val Arg Gly Gly Leu Leu Tyr Gln Gly Ala Val Arg Leu 115 120 125

Ala Ala Gly Ala Gln Met Ala Ala Asp Cys Cys Ser Leu Tyr Trp Glu 130 135 140

Ser His 145

<210> 517

<211> 26

<212> PRT

<213> Homo sapiens

<400> 517

Tyr Pro Thr Leu Phe Trp Leu Cys Pro Ser Ala Val Ser Pro Trp Ala 1 5 10 15

Tyr Thr Cys Tyr Gln Leu Gly Leu Gly Pro
20 25

<210> 518

<211> 25

<212> PRT

<213> Homo sapiens

<400> 518

Asp Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp Phe Arg Gly Gly
1 5 10 15

Gly Val Thr Asn Cys Ser Gly Pro Gln
20 25

<210> 519

<211> 22

<212> PRT

<213> Homo sapiens

<400> 519

Leu Leu Tyr Gln Gly Ala Val Arg Leu Ala Ala Gly Ala Gln Met Ala 1 5 10 15

Ala Asp Cys Cys Ser Leu 20

<210> 520

<211> 155

<212> PRT

<213> Homo sapiens

<400> 520

Asn Lys Arg Lys Thr Tyr Leu Phe Leu Glu Val Gly Met Trp Gly Val 1 5 10 15

Gly Gln Asn Arg Trp Trp Pro Trp Glu Arg Val Pro Arg Gly Arg Gly
20 25 30

Trp Gly Cys Leu Ser Lys Glu Gly Gln Val Met Asn Arg Ala Ser Thr 35 40 45

Pro Ser Arg Gly Phe Leu Gly Pro Pro Lys His Trp Ala Lys Thr Trp 50 55 60

Lys Leu Gly Ile Asp Lys Val Gln Arg Asp Val Gly Asn Ser Ala Cys 65 70 75 80

Gly Pro Ala His Thr Glu Gln Gly Pro Phe Val Glu Gly Arg Trp Lys

85

90

95

Val Met Ser Trp Gly Trp Ala Pro Gly Ser Pro Trp Ile Met Pro Gln
100 105 110

Gly Arg Ser Ser Asn Thr Gly Leu Phe Arg Val Arg Lys Arg Met 115 120 125

Thr Gly Leu Pro Ser Cys Thr Leu Gly Phe Pro Phe Ile Ser Thr Ala 130 135 140

Arg Arg Ser Pro Leu Gly Ser Gln Thr Met Glu 145 150 155

<210> 521

<211> 26

<212> PRT

<213> Homo sapiens

<400> 521

.Gly Val Gly Gln Asn Arg Trp Trp Pro Trp Glu Arg Val Pro Arg Gly
1 5 10 15

Arg Gly Trp Gly Cys Leu Ser Lys Glu Gly 20 25

<210> 522

<211> 26

<212> PRT

232 <213> Homo sapiens <400> 522 Ala Lys Thr Trp Lys Leu Gly Ile Asp Lys Val Gln Arg Asp Val Gly Asn Ser Ala Cys Gly Pro Ala His Thr Glu <210> 523 <211> 42 <212> PRT <213> Homo sapiens <400> 523 Trp Ala Pro Gly Ser Pro Trp Ile Met Pro Gln Gly Arg Ser Ser Asn Thr Gly Leu Phe Arg Val Arg Lys Arg Arg Met Thr Gly Leu Pro Ser 25 Cys Thr Leu Gly Phe Pro Phe Ile Ser Thr <210> 524 <211> 17 <212> PRT <213> Homo sapiens <400> 524 Ser Ser Tyr Gln Cys Pro Lys Val Thr Phe Phe Lys Ser Ser Val Asp 5 Thr <210> 525 <211> 14 <212> PRT <213> Homo sapiens <400> 525 Tyr Ile Tyr Ser Tyr Leu Gly Phe Phe Asn Gln Ile Asn Lys 5 <210> 526 <211> 6 <212> PRT

SUBSTITUTE SHEET (RULE 26)

<213> Homo sapiens

Ala Arg Asp Leu Ile Leu

<400> 526

<210> 527

<211> 43

<212> PRT

<213> Homo sapiens

<400> 527

Leu Thr Phe Tyr Leu Gln Phe Leu Ala Pro Lys Asp Lys Pro Ser Gly 1 5 10 15

Asp Thr Ala Ala Val Phe Glu Glu Gly Gly Asp Val Asp Asp Leu Val
20 25 30

Ser Thr Phe Asn Met His Leu Val Phe Cys Asp 35

<210> 528

<211> 25

<212> PRT

<213> Homo sapiens

<400> 528

Phe Leu Ala Pro Lys Asp Lys Pro Ser Gly Asp Thr Ala Ala Val Phe
1 5 10 15

Glu Glu Gly Gly Asp Val Asp Asp Leu 20 25

<210> 529

<211> 13

<212> PRT

<213> Homo sapiens

<400> 529

Ala Arg Ala Gly Ala Lys Ile Leu Phe Glu Gly Glu Phe
1 5 10

<210> 530

<211> 92

<212> PRT

<213> Homo sapiens

<400> 530

Asn Phe Glu Ile His Ser Ala Phe Pro Phe Met Leu Phe Val Ala Cys

1 10 15

Leu Leu His Ser Ser Cys Pro Arg Thr Ala Arg Phe Leu Ala Ser Pro 20 25 30

Leu Ser Glu Ser Asn Val Ile Phe Tyr Gln Asn Gln Tyr Gln Phe Pro

Cys Ile Leu Cys Phe Ile Glu Phe Ala Arg Leu Thr Ser Phe Lys His

50 55

Leu Ile His Ser Gln Ser His Leu Val Arg Leu Gln Tyr Glu Asp Phe 70 75

Ser Val Ser Ser Glu Ala Trp Asp Thr Glu Leu Thr 85

<210> 531

<211> 26

<212> PRT

<213> Homo sapiens

<400> 531

Phe Pro Phe Met Leu Phe Val Ala Cys Leu Leu His Ser Ser Cys Pro 5

Arg Thr Ala Arg Phe Leu Ala Ser Pro Leu 20

<210> 532

<211> 26

<212> PRT

<213> Homo sapiens

<400> 532

Asn Val Ile Phe Tyr Gln Asn Gln Tyr Gln Phe Pro Cys Ile Leu Cys 10

Phe Ile Glu Phe Ala Arg Leu Thr Ser Phe 20

<210> 533

<211> 23

<212> PRT

<213> Homo sapiens

<400> 533

Ser Gln Ser His Leu Val Arg Leu Gln Tyr Glu Asp Phe Ser Val Ser 10

Ser Glu Ala Trp Asp Thr Glu

<210> 534

<211> 10

<212> PRT

<213> Homo sapiens

<400> 534

Gln Lys Phe Leu Cys Ala Ser Asp Gly Asp 5

```
<210> 535
  <211> 177
  <212> PRT
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (160)
  <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
 <222> (162)
 <223> Xaa equals any of the naturally occurring L-amino acids
 <400> 535
 Ala Glu Val Pro Leu Arg Val Arg Arg Arg His Gly Arg Pro His Gly
 Pro Gly Gly Arg Gln Leu Ala Leu Gly Ile Pro Ala Leu Arg Ser Leu
 Pro Gly Cys Val Pro Arg His His Gly Cys Ser Pro Gly Tyr Gly Cys
          35
 Leu His Arg Arg Ile Leu Cys Leu Pro Leu Ile Leu Leu Val Tyr
Lys Gln Arg Gln Ala Ala Ser Asn Arg Arg Ala Gln Glu Leu Val Arg
                     70
                                         75
Met Asp Ser Asn Ile Gln Gly Ile Glu Asn Pro Gly Phe Glu Ala Ser
Pro Pro Ala Gln Gly Ile Pro Glu Ala Lys Val Arg His Pro Leu Ser
                                105
Tyr Val Ala Gln Arg Gln Pro Ser Glu Ser Gly Arg His Leu Leu Ser
        115
                            120
Glu Pro Ser Thr Pro Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe
Pro Ser Leu Asp Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile Xaa
145
                                        155
Pro Xaa Trp Gly Thr Val Gly Cys Cys Gly Trp Val Trp Gly Arg Cys
Ile
```

<210> 536

<211> 27

<212> PRT

<213> Homo sapiens

<400> 536

Gly Pro Gly Gly Arg Gln Leu Ala Leu Gly Ile Pro Ala Leu Arg Ser 10

Leu Pro Gly Cys Val Pro Arg His His Gly Cys 20

<210> 537

<211> 25

<212> PRT

<213> Homo sapiens

<400> 537

Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu Ala Lys Val Arg

His Pro Leu Ser Tyr Val Ala Gln Arg

<210> 538

<211> 88

<212> PRT

<213> Homo sapiens

<400> 538

Asp Met Ser Leu Gly Met Trp Gln His Gln Trp Asp Lys Met Asp Thr

Gly Pro Pro Ser Gln Ala Pro Asp Thr Gly His Gly Gly Glu Thr Ser 25

Pro Pro Trp His Ala Leu Gly Ser Pro Val Leu Pro Glu Ala Ala Leu 40

Leu Ser Asp Phe Leu Phe Val Pro Gln Trp Leu Trp Gly Gln Ala Cys

Leu Pro Thr Gly His Arg His Leu Pro Gln Leu Pro Pro Thr Ser Ser 65 70

Phe Ser Glu Asp Leu Ser Thr Gly

85

<210> 539

<211> 78

<212> PRT

<213> Homo sapiens

<400> 539

Pro Val Asp Arg Ser Ser Glu Lys Leu Leu Val Gly Gly Ser Trp Gly 5

237

Arg Trp Arg Trp Pro Val Gly Arg Gln Ala Trp Pro Gln Ser His Cys
20 25 30

Gly Thr Lys Arg Lys Ser Asp Arg Arg Ala Ala Ser Gly Lys Thr Gly 35 40 45

Glu Pro Ser Ala Cys His Gly Gly Glu Val Ser Pro Pro Cys Pro Val
50 55 60

Ser Gly Ala Trp Glu Gly Gly Pro Val Ser Ile Leu Ser His
65 70 75

<210> 540

<211> 22

<212> PRT

<213> Homo sapiens

<400> 540

Pro Val Asp Arg Ser Ser Glu Lys Leu Leu Val Gly Gly Ser Trp Gly

1 5 10 15

Arg Trp Arg Trp Pro Val
20

<210> 541

<211> 25

<212> PRT

<213> Homo sapiens

<400> 541

Thr Lys Arg Lys Ser Asp Arg Arg Ala Ala Ser Gly Lys Thr Gly Glu

1 5 10 15

Pro Ser Ala Cys His Gly Gly Glu Val

<210> 542

<211> 46

<212> PRT

<213> Homo sapiens

<400> 542

Met Thr Ser Lys Phe Gly Glu Ser Gly Thr Gly Ser Arg Asp Gly Lys

1 5 10 15

Lys Thr Ser Pro Gly Pro Gly Gly Asp Arg Gly Val Leu Gly Ser Glu 20 25 30

Ser Arg Cys Arg Pro Asp Ser Glu Gly Cys Arg Trp Ala Thr 35 40 45

<210> 543

<211> 20

<212> PRT

<213> Homo sapiens

<400> 543

Ser Pro Gly Pro Gly Gly Asp Arg Gly Val Leu Gly Ser Glu Ser Arg

Cys Arg Pro Asp

<210> 544

<211> 23

<212> PRT

<213> Homo sapiens

<400> 544

Pro Pro Ser Gln Ala Pro Asp Thr Gly His Gly Gly Glu Thr Ser Pro

Pro Trp His Ala Leu Gly Ser

<210> 545

<211> 15

<212> PRT

<213> Homo sapiens

<400> 545

His Glu Val Gln Pro Ser Tyr Leu Pro Ser Asn Ser Gly Leu Ile

<210> 546

<211> 22

<212> PRT

<213> Homo sapiens

<400> 546

Leu Arg Ile Ser Val Leu Cys Arg Glu Thr Ala Cys Asn Trp Ser His

His Pro Leu Asp Ser Asn

20

<210> 547

<211> 32

<212> PRT

<213> Homo sapiens

<400> 547

Leu Thr Val Thr Val Arg Asn Pro Gly Ser Thr His Ala Ser Gly Arg 5

Pro Arg Arg Ser Gly Val Trp Ala Arg Arg Gly Leu Val Trp Gln

SUBSTITUTE SHEET (RULE 26)

20

25

30

```
<210> 548
 <211> 38
 <212> PRT
 <213> Homo sapiens
 <400> 548
 Thr Pro Cys Ser Ala Gln Phe Ser Val Leu Gly Pro Ser Gly Pro Ile
 Leu Ala Met Val Gly Glu Asp Ala Asp Leu Pro Cys His Leu Phe Pro
                                  25
 Thr Met Ser Ala Glu Thr
          35
 <210> 549
 <211> 60
 <212> PRT
 <213> Homo sapiens
 <400> 549
Met Glu Leu Lys Trp Val Ser Ser Ser Leu Arg Gln Val Val Asn Val
Tyr Ala Asp Gly Lys Glu Val Glu Asp Arg Gln Ser Ala Pro Tyr Arg
Gly Arg Thr Ser Ile Leu Arg Asp Gly Ile Thr Ala Gly Lys Ala Ala
         35
Leu Arg Ile His Asn Val Thr Ala Ser Asp Ser Gly
                         55
<210> 550
<211> 26
<212> PRT
<213> Homo sapiens
Leu Glu Val Lys Gly Tyr Glu Asp Gly Gly Ile His Leu Glu Cys Arg
                  5
Ser Thr Gly Trp Tyr Pro Gln Pro Gln Ile
             20
```

<210> 551 <211> 80 <212> PRT

240

<213> Homo sapiens

<400> 551

Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val Ser Leu 1 5 10 15

Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser Val Leu 20 25 30

Gly Pro Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala Asp Leu 35 40 45

Pro Cys His Leu Phe Pro Thr Met Ser Ala Glu Thr Met Glu Leu Lys 50 55 60

Trp Val Ser Ser Ser Leu Arg Gln Val Val Asn Val Tyr Ala Asp Gly 65 70 75 80

<210> 552

<211> 103

<212> PRT

<213> Homo sapiens

<400> 552

Arg His Glu Leu Ser His Asn Arg Lys Asn Gly Glu Leu Leu Ile Asp
1 5 10 15

Arg Leu Tyr Ser Val Gly Ser Asp Ser Pro Met Gly Ile Pro Arg Asp
20 25 30

Ile Ile Phe Thr Asp Gly Phe Pro Tyr Trp Asn Pro Lys Val Lys Thr 35 40 45

Leu Lys Asp Arg His Phe Trp Gln Ser Ile Asp Glu Asn Gly Lys Phe 50 60

Pro Gly Phe Pro Ser Ala Gln Leu Ser Cys Leu Pro Pro Leu Gly Pro 65 70 75 80

Ala Ala His Ser Leu Leu Ser Ser Val Phe Cys Ala Trp Thr Leu Trp 85 90 95

Ala His Pro Gly His Gly Gly 100

<210> 553

<211> 24

<212> PRT

<213> Homo sapiens

<400> 553

Leu Leu Ile Asp Arg Leu Tyr Ser Val Gly Ser Asp Ser Pro Met Gly

241

1 5 10 15

Ile Pro Arg Asp Ile Ile Phe Thr 20

<210> 554

<211> 25

<212> PRT

<213> Homo sapiens

<400> 554

Asn Pro Lys Val Lys Thr Leu Lys Asp Arg His Phe Trp Gln Ser Ile

1 5 10 15

Asp Glu Asn Gly Lys Phe Pro Gly Phe 20 25

<210> 555

<211> 24

<212> PRT

<213> Homo sapiens

<400> 555

Leu Gly Pro Ala Ala His Ser Leu Leu Ser Ser Val Phe Cys Ala Trp

1 5 10 15

Thr Leu Trp Ala His Pro Gly His

<210> 556

<211> 135

<212> PRT

<213> Homo sapiens

<400> 556

Arg Leu Gln His Trp Val Leu Ile Phe Thr Leu Glu Val Lys Gly Tyr

1 5 10 15

Glu Asp Gly Gly Ile His Leu Glu Cys Arg Ser Thr Gly Trp Tyr Pro
20 25 30

Gln Pro Gln Ile Gln Trp Ser Asn Ala Lys Gly Glu Asn Ile Pro Ala 35 40 45

Val Glu Ala Pro Val Val Ala Asp Gly Val Gly Leu Tyr Glu Val Ala 50 55 60

Ala Ser Val Ile Met Arg Gly Gly Ser Gly Glu Gly Val Ser Cys Ile
65 70 75 80

Ile Arg Asn Ser Leu Leu Gly Leu Glu Lys Thr Ala Ser Ile Ser Ile 85 90 95

Ala Asp Pro Ser Ser Gly Ala Pro Ser Pro Gly Ser Gln Pro Trp Gln

SUBSTITUTE SHEET (RULE 26)

242

100 105 110

Gly Pro Cys Leu Ser Cys Cys Cys Phe Ser Pro Glu Pro Val Thr Ser 115 120 125

Cys Gly Asp Asn Arg Arg Lys 130 135

<210> 557

<211> 25

<212> PRT

<213> Homo sapiens

<400> 557

Gly Gly Ile His Leu Glu Cys Arg Ser Thr Gly Trp Tyr Pro Gln Pro 1 5 10 15

Gln Ile Gln Trp Ser Asn Ala Lys Gly
20 25

<210> 558

<211> 27

<212> PRT

<213> Homo sapiens

<400> 558

Pro Gln Ile Gln Trp Ser Asn Ala Lys Gly Glu Asn Ile Pro Ala Val 1 5 10 15

Glu Ala Pro Val Val Ala Asp Gly Val Gly Leu

<210> 559

<211> 27

<212> PRT

<213> Homo sapiens

<400> 559

Asn Ile Pro Ala Val Glu Ala Pro Val Val Ala Asp Gly Val Gly Leu

1 5 10 15

Tyr Glu Val Ala Ala Ser Val Ile Met Arg Gly
20 25

<210> 560

<211> 27

<212> PRT

<213> Homo sapiens

<400> 560

Ser Gly Ala Pro Ser Pro Gly Ser Gln Pro Trp Gln Gly Pro Cys Leu

1 5 10 15

Ser Cys Cys Phe Ser Pro Glu Pro Val Thr 20 25

<210> 561

<211> 131

<212> PRT

<213> Homo sapiens

<400> 561

Ser Ser Ser Ile Cys Asp His Glu Arg Arg Leu Arg Gly Gly Cys Ile
1 5 10 15

Leu His His Gln Lys Phe Pro Pro Arg Pro Gly Lys Asp Ser Gln His 20 25 30

Phe His Arg Arg Pro Phe Phe Arg Ser Ala Gln Pro Trp Ile Ala Ala 35 40 45

Leu Ala Gly Thr Leu Pro Ile Leu Leu Leu Leu Leu Ala Gly Ala Ser 50 55 60

Tyr Phe Leu Trp Arg Gln Gln Lys Glu Ile Thr Ala Leu Ser Ser Glu 65 70 75 80

Ile Glu Ser Glu Gln Glu Met Lys Glu Met Gly Tyr Ala Ala Thr Glu 85 90 95

Arg Glu Ile Ser Leu Arg Glu Ser Leu Gln Glu Glu Leu Lys Arg Lys
100 105 110

Lys Ile Gln Tyr Leu Thr Arg Gly Glu Glu Ser Ser Ser Asp Thr Asn 115 120 125

Lys Ser Ala 130

<210> 562

<211> 28

<212> PRT

<213> Homo sapiens

<400> 562

Lys Asp Ser Gln His Phe His Arg Arg Pro Phe Phe Arg Ser Ala Gln
1 5 10 15

Pro Trp Ile Ala Ala Leu Ala Gly Thr Leu Pro Ile 20 25

<210> 563

<211> 28

<212> PRT

<213> Homo sapiens

<400> 563

244

Glu Ile Glu Ser Glu Gln Glu Met Lys Glu Met Gly Tyr Ala Ala Thr 1 5 10 15

Glu Arg Glu Ile Ser Leu Arg Glu Ser Leu Gln Glu 20 25

<210> 564

<211> 33

<212> PRT

<213> Homo sapiens

<400> 564

Val Asn Asn Met Ile Ala Phe Tyr Ser Ala Arg Asp Ser Tyr Val Tyr

1 5 10 15

Pro His Phe Ser Gly Glu Glu Met Leu Gln Met Arg Leu His Leu Val 20 25 30

Lys

<210> 565

<211> 38

<212> PRT

<213> Homo sapiens

<400> 565

Thr Pro Cys Ser Ala Gln Phe Ser Val Leu Gly Pro Ser Gly Pro Ile
1 5 10 15

Leu Ala Met Val Gly Glu Asp Ala Asp Leu Pro Cys His Leu Phe Pro
20 25 30

Thr Met Ser Ala Glu Thr 35

<210> 566

<211> 23

<212> PRT

<213> Homo sapiens

<400> 566

Lys Trp Val Ser Ser Ser Leu Arg Gln Val Val Asn Val Tyr Ala Asp 1 5 10 15

Gly Lys Glu Val Glu Asp Arg 20

<210> 567

<211> 25

<212> PRT

<213> Homo sapiens

WO 99/31117 PCT/US98/27059 245 <400> 567 Arg Thr Ser Ile Leu Arg Asp Gly Ile Thr Ala Gly Lys Ala Ala Leu Arg Ile His Asn Val Thr Ala Ser Asp <210> 568 <211> 23 <212> PRT <213> Homo sapiens <400> 568 Cys Tyr Phe Gln Asp Gly Asp Phe Tyr Glu Lys Ala Leu Val Glu Leu Lys Val Ala Ala Leu Gly Ser 20 <210> 569 <211> 23 <212> PRT <213> Homo sapiens <400> 569 Gly Tyr Glu Asp Gly Gly Ile His Leu Glu Cys Arg Ser Thr Gly Trp Tyr Pro Gln Pro Gln Ile Gln 20 <210> 570 <211> 23 <212> PRT <213> Homo sapiens <400> 570 Asn Ile Pro Ala Val Glu Ala Pro Val Val Ala Asp Gly Val Gly Leu 10 Tyr Glu Val Ala Ala Ser Val 20

<210> 571 <211> 21

<212> PRT

<213> Homo sapiens

<400> 571

Gln Gln Lys Glu Ile Thr Ala Leu Ser Ser Glu Ile Glu Ser Glu Gln
1 5 10 15

Glu Met Lys Glu Met

PCT/US98/27059

20

```
<210> 572
 <211> 24
  <212> PRT
 <213> Homo sapiens
 <400> 572
 Leu Arg Glu Ser Leu Gln Glu Glu Leu Lys Arg Lys Lys Ile Gln Tyr
 Leu Thr Arg Gly Glu Glu Ser Ser
             20
 <210> 573
 <211> 13
 <212> PRT
 <213> Homo sapiens
 <400> 573
 Gly Glu Glu Met Leu Gln Met Arg Leu His Leu Val Lys
            5
 <210> 574
 <211> 40
 <212> PRT
 <213> Homo sapiens
 <400> 574
Ser Ala Gln Phe Ser Val Leu Gly Pro Ser Gly Pro Ile Leu Ala Met
                  5
Val Gly Glu Asp Ala Asp Leu Pro Cys His Leu Phe Pro Thr Met Ser
                                 25
Ala Glu Thr Met Glu Leu Lys Trp
              40
<210> 575
<211> 12
<212> PRT
<213> Homo sapiens
<400> 575
Pro Gln Gly Gly Leu Thr Leu Pro Ser Val Trp Gly
                  5
<210> 576
<211> 106
<212> PRT
<213> Homo sapiens
```

<400> 576

Gly Gly Pro Cys His Leu Trp Leu Leu Gly Pro Arg Arg Thr Gln Leu 1 5 10 15

Pro Gly Arg Arg Ala Ser Leu Pro Phe Arg Ser Gln Gly Glu Leu Thr 20 25 30

Gln Ala Phe Leu Gly Leu Trp Lys His Gln Met Pro Ala Leu Thr 35 40 45

Gln Glu Gln Gln Val Arg Ala Glu Arg Arg Arg Glu Ala Val Arg Met 50 55 60

Glu Ile Pro Gly Leu Phe Phe Ala Ser Leu Ala Asn Trp Gly Leu Leu 65 70 75 80

Tyr Arg Thr Ser Gln Asp Phe Ile Ser Pro Tyr Leu Cys Ala Ala Pro 85 90 95

Ser Thr Pro His Pro Pro Leu Gly Gly Pro 100 105

<210> 577

<211> 23

<212> PRT

<213> Homo sapiens

<400> 577

Gly Pro Arg Arg Thr Gln Leu Pro Gly Arg Arg Ala Ser Leu Pro Phe
1 5 10

Arg Ser Gln Gly Glu Leu Thr 20

<210> 578

<211> 24

<212> PRT

<213> Homo sapiens

<400> 578

Gln Met Pro Ala Leu Thr Gln Glu Gln Gln Val Arg Ala Glu Arg Arg

1 5 10 15

Arg Glu Ala Val Arg Met Glu Ile 20

<210> 579

<211> 25

<212> PRT

<213> Homo sapiens

<400> 579

Ala Asn Trp Gly Leu Leu Tyr Arg Thr Ser Gln Asp Phe Ile Ser Pro 1 5 10

SUBSTITUTE SHEET (RULE 26)

```
Tyr Leu Cys Ala Ala Pro Ser Thr Pro
             20
 <210> 580
 <211> 34
 <212> PRT
 <213> Homo sapiens
 <400> 580
 Leu Ser Phe Lys Asp Lys Ser Thr Tyr Ile Glu Ser Ser Thr Lys Val
Tyr Asp Asp Met Ala Phe Arg Tyr Leu Ser Trp Ile Leu Phe Pro Leu
                                 25
Leu Gly
<210> 581
<211> 31
<212> PRT
<213> Homo sapiens
<400> 581
Leu Leu Thr Phe Gly Phe Ile Thr Met Thr Pro Gln Leu Phe Ile Asn
Tyr Lys Leu Lys Ser Val Ala His Leu Pro Trp Arg Met Leu Thr
             20 25
<210> 582
<211> 30
<212> PRT
<213> Homo sapiens
<400> 582
Thr Tyr Lys Ala Leu Asn Thr Phe Ile Asp Asp Leu Phe Ala Phe Val
Ile Lys Met Pro Val Met Tyr Arg Ile Gly Cys Leu Arg Asp
             20
<210> 583
<211> 30
<212> PRT
<213> Homo sapiens
<400> 583
Asp Val Val Phe Phe Ile Tyr Leu Tyr Gln Arg Trp Ile Tyr Arg Val
Asp Pro Thr Arg Val Asn Glu Phe Gly Met Ser Gly Glu Asp
```

249

20 25 30

<210> 584

<211> 44

<212> PRT

<213> Homo sapiens

<400> 584

Val Ala Gly Ile Phe Pro Arg Leu Ser Phe Lys Asp Lys Ser Thr Tyr

1 5 10 15

Ile Glu Ser Ser Thr Lys Val Tyr Asp Asp Met Ala Phe Arg Tyr Leu 20 25 30

Ser Trp Ile Leu Phe Pro Leu Leu Gly Cys Tyr Ala 35 40

<210> 585

<211> 19

<212> PRT

<213> Homo sapiens

<400> 585

Trp Ala Ala Met Pro Ser Thr Val Phe Cys Thr Trp Ser Thr Arg Ala
1 5 10 15

Gly Thr Pro

<210> 586

<211> 28

<212> PRT

<213> Homo sapiens

<400> 586

Pro Trp Val Ala Gly Ile Phe Pro Arg Leu Ser Phe Lys Asp Lys Ser 1 5 10 15

Thr Tyr Ile Glu Ser Ser Thr Lys Val Tyr Asp Asp

<210> 587

<211> 88

<212> PRT

<213> Homo sapiens

<400> 587

Ala Gly Glu Asp Ser Cys His Pro Val Leu Ser Val Gln Pro Asp Val

1 5 10 15

His Asp Leu Gly Trp Gln Glu Ser Ser Pro Ala Tyr Pro Ser Arg Thr
20 25 30

250

Ser Pro Arg Ile Ser Ser Pro Arg Pro Lys Cys Met Met Ile Trp His
35 40 45

Ser Gly Thr Cys Pro Gly Ser Ser Ser Arg Ser Trp Ala Ala Met Pro 50 55 60

Ser Thr Val Phe Cys Thr Trp Ser Thr Arg Ala Gly Thr Pro Gly Cys 65 70 75 80

Ser Ala Cys Ser Thr Ala Ser Cys

<210> 588

<211> 30

<212> PRT

<213> Homo sapiens

<400> 588

Leu Ser Val Gln Pro Asp Val His Asp Leu Gly Trp Gln Glu Ser Ser

1 10 15

Pro Ala Tyr Pro Ser Arg Thr Ser Pro Arg Ile Ser Ser Pro
20 25 30

<210> 589

<211> 25

<212> PRT

<213> Homo sapiens

<400> 589

Gly Ser Ser Ser Arg Ser Trp Ala Ala Met Pro Ser Thr Val Phe Cys

1 10 15

Thr Trp Ser Thr Arg Ala Gly Thr Pro 20 25

<210> 590

<211> 22

<212> PRT

<213> Homo sapiens

<400> 590

Cys Tyr Ala Val Tyr Ser Leu Leu Tyr Leu Glu His Lys Gly Trp Tyr 1 5 10 15

Ser Trp Val Leu Ser Met

20

<210> 591

<211> 12

<212> PRT

<213> Homo sapiens

```
251
 <400> 591
 Leu Gly Glu Phe Leu Ser Ser Gln Cys Phe Leu Pro
                  5
 <210> 592
 <211> 20
 <212> PRT
 <213> Homo sapiens
 <400> 592
 Arg Ser Arg Arg Asn Arg Val Ala Met Gly Met Trp Ala Ser Leu Asp
 Ala Leu Trp Glu
 <210> 593
 <211> 92
 <212> PRT
 <213> Homo sapiens
 <400> 593
Pro Arg Val Arg Cys Gln Gln Arg Ala Glu Gly Gly Met Gly Ala Gly
Ile Gly Val Gly Pro Ser Glu Arg Thr Asp Ile Ala Val Thr Pro Arg
Gly Arg Ser Glu Gly Ala Ser Val Gly Val Ala Pro Val His Ala Glu
Gly Ala Gly Gly Thr Gly Trp Pro Trp Gly Cys Gly His Arg Trp Thr
Leu Cys Gly Arg Cys Arg Pro Arg Ser Val Ser Ser Gly Pro Cys Cys
 65
                      70
Ser Phe Pro Gly Gln Cys Ile Phe Gly Arg Pro Ser
                  85
<210> 594
<211> 24
<212> PRT
<213> Homo sapiens
Gly Gly Met Gly Ala Gly Ile Gly Val Gly Pro Ser Glu Arg Thr Asp
                  5
                                     10
```

<210> 595

Ile Ala Val Thr Pro Arg Gly Arg
20

<211> 26

<212> PRT

<213> Homo sapiens

<400> 595

Gly Cys Gly His Arg Trp Thr Leu Cys Gly Arg Cys Arg Pro Arg Ser 1 5 10 15

Val Ser Ser Gly Pro Cys Cys Ser Phe Pro 20 25

<210> 596

<211> 24

<212> PRT

<213> Homo sapiens

<400> 596

Lys Lys His Gly Phe Asn Gln Gln Thr Leu Gly Phe Phe Thr Trp Lys

1 10 15

Tyr Asn Lys Asn Leu Val

<210> 597

<211> 21

<212> PRT

<213> Homo sapiens

<400> 597

Pro Lys Leu Pro Cys Ser Pro Ala Glu Gly His Thr Ser Leu Gly
1 5 10 15

Pro Leu Leu Pro Phe 20

<210> 598

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 598

Ala Ser Leu Glu Leu Xaa Pro Ser Lys Ser Gln Leu Ser Thr Glu Trp

1 5 10 15

Gly Phe Thr Trp Ile Val Gly Leu Gly Met Ser Pro Ser Thr Ala Leu 20 25 30

Trp Thr Glu Cys Thr Cys Thr Pro Phe Leu Val Leu Leu Ser His Ala
35 40 45

SUBSTITUTE SHEET (RULE 26)

```
Ser Gly His Phe Phe Trp Leu Ser Pro Leu Ala Ser Leu Val Ile Pro 50 55 60
```

Pro Val Thr Asp Arg Lys 65 70

<210> 599

<211> 32

<212> PRT

<213> Homo sapiens

<400> 599

Trp Gly Phe Thr Trp Ile Val Gly Leu Gly Met Ser Pro Ser Thr Ala 1 5 10 15

Leu Trp Thr Glu Cys Thr Cys Thr Pro Phe Leu Val Leu Leu Ser His 20 25 30

<210> 600

<211> 106

<212> PRT

<213> Homo sapiens

<400> 600

Val Ala Val Gly Val Cys Arg Glu Asp Val Met Gly Ile Thr Asp Arg

Ser Lys Met Ser Pro Asp Val Gly Ile Trp Ala Ile Tyr Trp Ser Ala 20 25 30

Ala Gly Tyr Trp Pro Leu Ile Gly Phe Pro Gly Thr Pro Thr Gln Gln 35 40 45

Glu Pro Ala Leu His Arg Val Gly Val Tyr Leu Asp Arg Gly Thr Gly 50 55 60

Asn Val Ser Phe Tyr Ser Ala Val Asp Gly Val His Leu His Thr Phe 65 70 75

Ser Cys Ser Ser Val Ser Arg Leu Arg Pro Phe Phe Leu Val Glu Ser 85 90 95

Ile Ser Ile Phe Ser His Ser Thr Ser Asp 100 105

<210> 601

<211> 27

<212> PRT

<213> Homo sapiens

```
254
 <400> 601
 Ile Thr Asp Arg Ser Lys Met Ser Pro Asp Val Gly Ile Trp Ala Ile
 Tyr Trp Ser Ala Ala Gly Tyr Trp Pro Leu Ile
 <210> 602
 <211> 30
 <212> PRT
 <213> Homo sapiens
 <400> 602
 Arg Gly Thr Gly Asn Val Ser Phe Tyr Ser Ala Val Asp Gly Val His
 Leu His Thr Phe Ser Cys Ser Ser Val Ser Arg Leu Arg Pro
 <210> 603
 <211> 11
 <212> PRT
 <213> Homo sapiens
 <400> 603
Gly Thr Arg Gly Leu Gln Asn His Arg Thr Glu
<210> 604
<211> 6
<212> PRT
<213> Homo sapiens
<400> 604
Glu Leu Ser Gly Leu Gly
  1
<210> 605
<211> 6
<212> PRT
<213> Homo sapiens
<400> 605
Met Asp Asp Ile Lys Ile
 1
             5
<210> 606
<211> 57
<212> PRT
<213> Homo sapiens
```

<400> 606

255

Asn Phe Cys Val Ser Lys Asn Thr Phe Asn Arg Val Lys Arg Pro Ile
1 5 10 15

Lys Trp Val Lys Ile Phe Ala Asn Asp Ile Ser Cys Lys Arg Leu Ile 20 25 30

Ser Arg Ile His Lys Glu Ile Leu Pro Phe Asn Asn Lys Lys Gln Pro 35 40 45

Asp Phe Lys Val Lys Lys Ser Arg Lys 50 55

<210> 607

<211> 30

<212> PRT

<213> Homo sapiens

<400> 607

Phe Asn Arg Val Lys Arg Pro Ile Lys Trp Val Lys Ile Phe Ala Asn 1 5 10 15

Asp Ile Ser Cys Lys Arg Leu Ile Ser Arg Ile His Lys Glu 20 25 30

<210> 608

<211> 15

<212> PRT

<213> Homo sapiens

<400> 608

Glu Thr Gln Met Ala Asn Lys Tyr Met Lys Arg Cys Ser Thr Leu
1 5 10 15

<210> 609

<211> 59

<212> PRT

<213> Homo sapiens

<400> 609

Val Ile Arg Glu Leu Gln Val Lys Ala Thr Arg Arg Cys His Tyr Thr 1 5 10 15

Pro Ile Lys Trp Ser Lys Ser Lys Thr Leu Ile Ser Ser Asn Ala Asp 20 25 30

Glu Tyr Val Glu Pro Thr Arg Thr Leu Ile His Cys Trp Trp Lys Cys 35 40 45

Lys Ile Val Gln Pro Leu Cys Lys Thr Ala Trp 50 55

<210> 610

<211> 22

<212> PRT

<213> Homo sapiens

<400> 610

Ala Thr Arg Arg Cys His Tyr Thr Pro Ile Lys Trp Ser Lys Ser Lys

1 10 15

256

PCT/US98/27059

Thr Leu Ile Ser Ser Asn 20

<210> 611

<211> 64

<212> PRT

<213> Homo sapiens

<400> 611

Glu Leu Ser Gly Leu Val Ile Ile Thr Ala Trp Ile Ile Leu Cys His 1 5 10 15

Ser Ser Ser Lys Asn Pro Val Gly Gly Arg Ile Gln Leu Ala Ile Ala 20 25 30

Ile Val Ile Thr Leu Phe Pro Phe Ile Ser Trp Val Tyr Ile Tyr Ile 35 40 45

Asn Lys Glu Met Arg Ser Ser Trp Pro Thr His Cys Lys Thr Val Ile 50 55 60

<210> 612

<211> 57

<212> PRT

<213> Homo sapiens

<400> 612

Gln Cys Pro Gln Gly Thr Glu Thr Glu Ala Gly Val Ser Val Pro Pro 1 5 10 15

Arg Lys Glu Gly Gly Pro Tyr Val Ala Gly Leu Thr Ala Pro His 20 25 30

Val Ala Gly Leu Thr Ala Pro Arg Arg Val Leu Arg Ala Met Ala Pro 35 40 45

Ala Leu Trp Arg Ala Cys Asn Gly Leu 50 55

<210> 613

<211> 32

<212> PRT

<213> Homo sapiens

<400> 613 His Ser Ser Ser Lys Asn Pro Val Gly Gly Arg Ile Gln Leu Ala Ile

Ala Ile Val Ile Thr Leu Phe Pro Phe Ile Ser Trp Val Tyr Ile Tyr 25

<210> 614

<211> 32

<212> PRT

<213> Homo sapiens

<400> 614

Arg Lys Glu Gly Gly Pro Tyr Val Ala Gly Leu Thr Ala Pro His 1 5

Val Ala Gly Leu Thr Ala Pro Arg Arg Val Leu Arg Ala Met Ala Pro 25

<210> 615

<211> 32

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (9)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 615

Pro Gly Arg Pro Thr Arg Pro Ala Xaa Ala Gly Leu Ser Ser Gly Gly 5

Ala Ala Gln Glu Ala Pro Gln Ala Asp Pro Arg Pro Trp Leu Ala Arg 20 25

<210> 616

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

```
<220>
 <221> SITE
 <222> (29)
 <223> Xaa equals any of the naturally occurring L-amino acids
 His Tyr Xaa Ser Thr Pro Gly Arg Val Pro Val Arg Gln Phe Ala Ala
 Ala Ser Thr Ser Gly Gly Pro Trp Val Pro Gly Gly Xaa Leu Glu Ala
 Pro Phe Gln Val Ala Pro Ser Leu Ser His Ser Thr Pro Val Phe Pro
                               40
 Gly Leu Ile
      50
 <210> 617
 <211> 22
 <212> PRT
 <213> Homo sapiens
 <400> 617
Ala Arg Gly Lys Tyr Glu Ser Ala Gln Pro Gly Gly Thr Gln Pro Glu
Pro Gly Leu Gly Ala Arg
<210> 618
<211> 24
<212> PRT
<213> Homo sapiens
<400> 618
Ser Cys Gly Ser Ser Arg Arg Ser Ala Lys Arg Ser Leu Thr Leu Lys
                 5
Leu Ile Asp Phe Ser His Arg Ile
             20
<210> 619
<211> 52
<212> PRT
<213> Homo sapiens
<400> 619
His Tyr Phe Leu Arg Thr Val Ser Gly Leu Ser Val Val Pro Val Ser
Leu Arg Cys Cys Met Cys Pro Pro Pro Cys Thr Gly Pro Ala Pro Ala
                                 25
```

```
Thr Ala His Ser Pro Phe Asp Pro Pro Ala Leu Pro Ile Gln Phe Glu
                               40
  Tyr Gln Gln Ala
       50
  <210> 620
  <211> 45
  <212> PRT
  <213> Homo sapiens
 <400> 620
 Gln Leu Glu Ala Glu Ile Glu Asn Leu Ser Trp Lys Val Glu Arg Ala
 Asp Ser Tyr Asp Arg Gly Asp Leu Glu Asn Gln Met His Ile Ala Glu
              20
                                   25
 Gln Arg Arg Arg Thr Leu Leu Lys Asp Phe His Asp Thr
                              40
 <210> 621
 <211> 24
 <212> PRT
 <213> Homo sapiens
 <400> 621
 Val Pro Val Ser Leu Arg Cys Cys Met Cys Pro Pro Pro Cys Thr Gly
                                      10
 Pro Ala Pro Ala Thr Ala His Ser
             20
<210> 622
<211> 25
<212> PRT
<213> Homo sapiens
Ser Trp Lys Val Glu Arg Ala Asp Ser Tyr Asp Arg Gly Asp Leu Glu
                  5
Asn Gln Met His Ile Ala Glu Gln Arg
             20
<210> 623
<211> 227
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
```

<222> (53)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 623

His Glu Ala Trp Leu Arg Ser Ala Gly Thr Arg Glu Pro Pro Arg Glu

1 5 10 15

Gln Arg Thr Arg Arg Gln Thr Ala Gln Leu Ala Leu Gln Val Pro
20 25 30

Ala Pro Ser Arg Thr Pro Pro Met Ala Thr Asp Val Phe Asn Ser Lys
35 40 45

Asn Leu Ala Val Xaa Ala Gln Lys Lys Ile Leu Gly Lys Met Val Ser 50 60

Lys Ser Ile Ala Thr Thr Leu Ile Asp Asp Thr Ser Ser Glu Val Leu 65 70 75 80

Asp Glu Leu Tyr Arg Val Thr Arg Glu Tyr Thr Gln Asn Lys Lys Glu 85 90 95

Ala Glu Lys Ile Ile Lys Asn Leu Ile Lys Thr Val Ile Lys Leu Ala 100 105 110

Ile Leu Tyr Arg Asn Asn Gln Phe Asn Gln Asp Glu Leu Ala Leu Met 115 120 125

Glu Lys Phe Lys Lys Lys Val His Gln Leu Ala Met Thr Val Val Ser 130 135 140

Phe His Gln Val Asp Tyr Thr Phe Asp Arg Asn Val Leu Ser Arg Leu 145 150 155 160

Leu Asn Glu Cys Arg Glu Met Leu His Gln Ile Ile Gln Arg His Leu 165 170 175

Thr Ala Lys Ser His Gly Arg Val Asn Asn Val Phe Asp His Phe Ser 180 185 190

Asp Cys Glu Phe Leu Ala Ala Leu Tyr Asn Pro Phe Gly Asn Phe Lys
195 200 205

Pro His Leu Gln Lys Leu Cys Asp Gly Ile Asn Lys Met Leu Asp Glu 210 215 220

Glu Asn Ile 225

<210> 624

<211> 52

<212> PRT

<213> Homo sapiens

<400> 624

His Glu Ala Trp Leu Arg Ser Ala Gly Thr Arg Glu Pro Pro Arg Glu

5 10 15

Gln Arg Thr Arg Arg Gln Thr Ala Gln Leu Ala Leu Gln Val Pro 25

Ala Pro Ser Arg Thr Pro Pro Met Ala Thr Asp Val Phe Asn Ser Lys 40

Asn Leu Ala Val 50

<210> 625

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 625

Xaa Ala Gln Lys Lys Ile Leu Gly Lys Met Val Ser Lys Ser Ile Ala

Thr Thr Leu Ile Asp Asp Thr Ser Ser Glu Val Leu Asp Glu Leu Tyr

Arg Val Thr Arg Glu Tyr Thr Gln Asn Lys Lys Glu Ala Glu Lys Ile 40

Ile

<210> 626

<211> 51

<212> PRT

<213> Homo sapiens

<400> 626

Lys Asn Leu Ile Lys Thr Val Ile Lys Leu Ala Ile Leu Tyr Arg Asn

Asn Gln Phe Asn Gln Asp Glu Leu Ala Leu Met Glu Lys Phe Lys Lys 20 25

Lys Val His Gln Leu Ala Met Thr Val Val Ser Phe His Gln Val Asp 35

Tyr Thr Phe 50

<210> 627 <211> 52

<212> PRT

<213> Homo sapiens

<400> 627

Asp Arg Asn Val Leu Ser Arg Leu Leu Asn Glu Cys Arg Glu Met Leu 1 5 10 15

His Gln Ile Ile Gln Arg His Leu Thr Ala Lys Ser His Gly Arg Val

Asn Asn Val Phe Asp His Phe Ser Asp Cys Glu Phe Leu Ala Ala Leu 35 40 45

Tyr Asn Pro Phe 50

<210> 628

<211> 23

<212> PRT

<213> Homo sapiens

<400> 628

Gly Asn Phe Lys Pro His Leu Gln Lys Leu Cys Asp Gly Ile Asn Lys

1 10 15

Met Leu Asp Glu Glu Asn Ile 20

International application No. PCT/US98/27059

A. CL	ASSISTED A CONTRACT ASSESSMENT ASSISTANCE AS			
The second of Separation with the second of				
IPC(6) :C07H 21/00; C12N 1/15, 1/21, 5/10, 15/11, 15/63 US CL :435/91.41, 320.1, 325, 252.3, 254.11; 536/23.1, 23.5, 24.31				
According	to International Patent Classification (IPC) or to be	oth national classification and IPC		
	LDS SEARCHED			
Minimum o	documentation searched (classification system follo	wed by classification symbols)		
II .	435/91.41, 320.1, 325, 252.3, 254.11; 536/23.1, 2			
	, 520.2, 525, 252.3, 254.11, 530/23.1, 2	3.3, 24.31		
Documenta	ation searched other than minimum documentation to	the extent that such documents are include	4:- at - 5 11	
l		and oxens may such documents are included	in the fields searched	
			•	
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)				
GENBANK, EMBL, SWISS-PROT, SPTREMBL, PIR,				
searched: SEQ ID NO: 11-20 & 125-134				
C. DOC	CUMENTS CONSIDERED TO BE RELEVANT			
Category*	Citation of January - 14 1 11 11			
Caugory	Citation of document, with indication, where	appropriate, of the relevant passages	Relevant to claim No.	
X	Database GenBank, US National Li	hrary of Medicine (Pathoods	1 7 10	
	MD, USA), No. AA133381, HILLI	FR et al 'Wachil March ECT	1, 7-10	
	Project', complete record, 27 Novem	nher 1006		
	, 140 VOI	1990.		
X	Database GenBank, US National Li	hrary of Medicine (Dothords	1 7 10	
	MD, USA), No. T12400, LIEW et a	d 'A catalogue of genes in the	1, 7-10	
	cardiovascular system as identified	hy expressed seguence to sel		
	complete record, 27 November 1996	by expressed sequence tags,		
	The first cooling of the composition of the control			
\mathbf{x}	Database GenBank, US National Li	hrary of Medicine (Retherds	1, 7-10	
	MD, USA), No. AA496982, HILLI	FR et al 'Washil-March EST	1, /-10	
ļ	MD, USA), No. AA496982, HILLIER et al. 'WashU-Merck EST Project 1997', complete record, 12 August 1997.			
j	,	and and in the same of the sam		
- 1				
1				
		1		
ļ				
		İ		
V Bueto	Account to the second s			
X Further documents are listed in the continuation of Box C. See patent family annex.				
	niel categories of cited documents;	"I" later document published after the intern	national filing date or priority	
'A" door to be	ment defining the general state of the art which is not considered s of particular relevance	date and not in conflict with the application the principle or theory underlying the in	ation but cited to understand	
'B' certi	er document published on or after the international filing date	"X" document of particular relevance; the	claimed invention cannot be	
'L* doou	ment which may throw doubts on priority plain(a) or which is	considered novel or cannot be considered when the document is taken alone	d to involve an inventive step	
speci	to establish the publication date of another citation or other ial reason (as specified)	"Y" document of particular relevance; the	laimed invention conner be	
O* doou	ment referring to an oral disclosure, use, exhibition or other	considered to involve an inventive at	on when the document is 1	
p ^o document published prior to the international filing data but later than		oeing ouvious to a person skilled in the	ert [
me p	riority date claimed	*A* document member of the same petent fa	m ily	
Date of the actual completion of the international search		Date of mailing of the international searc	h report	
M W P 22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2				
		23 MAR 1999		
dame and mailing address of the ISA/US Commissioner of Patents and Trademarks Authorized officer				
Box PCT		SCOTT TO PRIEBE		
Washington, I acsimile No.	D.C. 20231 (703) 305-3230	BOOT D. FRIEBE	<u> </u>	
	(***) 303*3430	Telephone No. (703) 308-0196		

International application No.
PCT/US98/27059

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
X	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. U14626, D'ALESSIO et al. 'Cloning vector pSVSport1', complete record, 24 May 1995.	1, 7-10
X	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. AJ000730, SPERANDEO et al. 'The full cDNA for the human cationic amino acid transporter 3 (HCAT3)', complete record, 02 December 1997.	1
X	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. R31044, HILLIER et al. 'The WashU-Merck EST Project', complete record, 28 April 1995.	1, 7-10
X	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. AA446873, HILLIER et al. 'WashU-Merck EST Project 1997', complete record, 03 June 1997.	1, 7-10
K	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. AA135715, HILLIER et al. 'WashU-Merck EST Project', complete record, 14 May 1997.	1, 7-10
ĸ	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. AA194015, HILLIER et al. 'WashU-Merck EST Project', complete record, 19 May 1997.	1, 7-10
C	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. R72850, HILLIER et al. 'The WashU-Merck EST Project', complete record, 02 June 1995.	1, 7-10
ζ	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. T60940, HILLIER et al. 'WashU-Merck EST Project', complete record, 13 February 1995.	1, 7-10
	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. H86863, HILLIER et al. 'The WashU-Merck EST Project', complete record, 21 November 1995.	1, 7-10
	··	

Form PCT/ISA/210 (continuation of second sheet)(July 1992)*

International application No. PCT/US98/27059

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)				
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:				
1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:				
2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:				
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).				
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)				
This International Searching Authority found multiple inventions in this international application, as follows:				
Please See Extra Sheet.				
1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.				
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.				
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:				
4. X No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-10, 21				
Remark on Protest The additional search fees were accompanied by the applicant's protest.				
No protest accompanied the payment of additional search fees.				

Form PCT/ISA/210 (continuation of first sheet(1))(July 1992)★

International application No. PCT/US98/27059

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

- Groups I-XXVII, claim(s) 1-10 and 21, drawn to a polynucleotide, vector comprising same, first claimed method of use, i.e. using polynucleotide to make a cell, and the cell made by the process. Claims 1-10 and 21 recite 114 independent polynucleotides (SEQ ID NO: 11-124 or encoding SEQ ID NO: 125-238). Group I consists of the first ten polynucleotides (SEQ ID NOs 11-20 or encoding SEQ ID NOs 125-134). Each of groups II-XXVII consists of up to four of the remaining 104 polynucleotides, in order.
- Groups XXVIII-CXLI, claim(s) 11, 12, 14-16 and 17 (first part), drawn to a polypeptide, a method of making the polypeptide and first claimed method of use, i.e. in treatment. These claims recite 114 independent polypeptides, each of groups XXVIII-CXLI consists of a single polypeptide as set forth in SEQ ID NOs 125-238, respectively.
- Groups CXLI-CCLV, claim(s) 13 and 19, drawn to an antibody to a polypeptide and the first claimed method of using same. These claims recite 114 independent antibodies to 114 independent polypeptides, each of groups CXLI-CCLV consists an antibody against a single polypeptide as set forth in SEQ ID NOs 125-238, respectively.
- Groups CCLVI-CCLXXXII, claim(s) 17(second part), drawn to an additional method of using a polynucleotide. Group CCLVI consists of methods reciting the first ten polynucleotides (SEQ ID NOs 11-20 or encoding SEQ ID NOs 125-134). Each of groups CCLVII-CCLXXXII pertains to up to four of the remaining 104 polynucleotides, in order.
- Groups CCLXXXIII-CCCIX, claim(s) 18, drawn to a second additional method of using a polynucleotide. Group CCLXXXIII consists of methods reciting the first ten polynucleotides (SEQ ID NOs 11-20 or encoding SEQ ID NOs 125-134). Each of groups CCLXXXIV-CCCIX pertains to up to four of the remaining 104 polynucleotides, in order.
- Groups CCCX-CDXXIII, claim(s) 20, drawn to an additional method of using the polypeptide. These claims recite 114 independent methods of using 114 independent polypeptides, each of groups CCCX-CDXXIII consists an antibody against a single polypeptide as set forth in SEQ ID NOs 125-238, respectively.
- Groups CDXXIV-CDL, claim 22, drawn to a third additional method of using a polynucleotide. Group CDXXIV consists of methods reciting the first ten polynucleotides (SEQ ID NOs 11-20 or encoding SEQ ID NOs 125-134). Each of groups CDXXV-CDL pertains to up to four of the remaining 53 polynucleotides, in order.
- Claim 23 is unsearchable and cannot be grouped as it is drawn to unknown and unspecified compounds.

 The inventions listed as Groups I-CDL do not relate to a single inventive concept under PCT Rule 13.1

 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

 Each of the corresponding polynucleotides, polypeptides and antibodies are independent products, with different uses and being structurally, biochemically and biologically different products. Additional or alternate methods of use are claimed for individual polynucleotides and polypeptides. 37 CFR 1.475(b) does not provide for unity of invention of more than 1 product or more than one method of using a product as a combination of invention having unity of

invention. However, with respect to groups drawn to independent polynucleotides or alternate methods of using same recited in the alternative, in accordance with 1192 O.G. 68 (19 November 1966) applicant is entitled to an initial search of inventions pertaining to the first ten independent polynucleotides recited, and may elect to pay an additional fee for each search of up to four additional independent polynucleotides. For additional method of using each of the independent polynucleotides, applicant may further elect to pay an additional fee for an additional search involving the first ten polynucleotides and each additional search involving up to four additional polynucleotides. With respect to groups pertaining to independent polypeptides or antibodies to the independent polypeptides, each product or method of use is an additional invention. An additional fee must be paid for search of each additional invention relating to polypeptides or antibodies against same. With respect to the relationship between the claimed polynucleotides and the claimed polypeptides, there is no one-to-one correspondence, i.e. no corresponding scope, between claims drawn to polypucleotides and their use and those drawn to polypeptides, antibodies and their use. Consequently, there is no special

technical feature linking the polynucleotides and the polypeptides or antibodies claimed.

Form PCT/ISA/210 (extra sheet)(July 1992)#